



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 105257

TO: Phillip Gabel
Location: CM-1/9E12
Art Unit: 1644
Wednesday, October 08, 2003

Case Serial Number: 09/155739

From: Edward Hart
Location: Biotech-Chem Library
CM1-6B02
Phone: 305-9203

edward.hart@uspto.gov

Search Notes

Examiner Gabel,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

x S Claim 11; Page 69; 105pp; English.

x The sequence encodes the mouse antibody 21.6 heavy chain variable region, $\text{H}\alpha$, directed against leukocyte adhesion molecule VLA-4. Cloned cDNA sequences of mouse 21.6, $\text{V}\beta$ and $\text{V}\gamma$ (AAG99889 and AAG99892) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAG99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L49, L58 and L69 in the human kappa LC VR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used for inhibiting adhesion of a leukocyte to an endothelial cell and for treating inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, menigitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating anti-idiotypic antibodies.

xx Sequence 123 AA;

Query Match 100.0%; Score 655; DB 16; Length 123;

Best Local Similarity 100.0%; Pred. No. 7.2e-53; Mismatches 0; Indels 0; Gaps 0; Matches 123; Conservative 0;

Qy 1 QVQLVQSGAEVKPGASKVSKASGNIKDTYIHWVQAPGQLEWGRIDPANGTYK 60

Db 1 QVQLVQSGAEVKPGASKVSKASGNIKDTYIHWVQAPGQLEWGRIDPANGTYK 60

Qy 61 DPKFQGRVITTAQTSASATAYMELSSLRSQEDAVYTCARSGTYYKGYAMDYWGQGTVY 120

Db 61 DPKFQGRVITTAQTSASATAYMELSSLRSQEDAVYTCARSGTYYKGYAMDYWGQGTVY 120

Qy 121 VSS 123

Db 121 VSS 123

Qy 121 VSS 123

Db 121 VSS 123

RESULT 2
AAR81333 standard; Protein: 142 AA.

xx AC AAR81333;

xx DT 23-MAR-1986 (first entry)

DE Human VLA-4 reshaped antibody 21.6 light heavy variable region.

xx Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;

kw antibody engineering.

os Homo sapiens.

xx key Peptide 1..19

ft Location/Qualifiers /note- "signal peptide"

ft Region 20..49 /note- "framework region 1"

ft Region 50..54 /note- "complementarity determining region 1"

ft Region 55..68 /note- "complementarity determining region 2"

ft Region 69..85 /note- "framework region 2"

ft Region 86..117 /note- "complementarity determining region 3"

ft Region 118..131 /note- "complementarity determining region 3"

ft Region 132..142 /note- "framework region 4"

ft

xx PN W09519790-A1.

xx PD 27-JUL-1995.

xx PF 25-JAN-1995; 95WO-US01219.

xx PR 25-JAN-1994; 94US-0186269.

xx PA (ATHE-) ATHENA NEUROSCIENCES INC.

xx PI Bendig MM, Jones TS, Leger OJ, Saldanha J;

xx DR WPI; 1995-269276/35.

xx DR N-PSDB; AAG99894.

xx PR New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating inflammatory disease.

xx PS Disclosure; Fig 11; 105pp; English.

xx CC The sequence represents the human reshaped antibody 21.6 heavy chain variable region against leukocyte adhesion molecule VLA-4.

cc Cloned cDNA sequences of mouse 21.6, $\text{V}\beta$ (AAG99892) and $\text{V}\gamma$ (AAG99889)

cc Regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (AAG99895-98) and then

cc subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized heavy chain, amino acids H27, H28, H29, H44 and H71 in the human HC VR

cc framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig H chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanised antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and to treat inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, menigitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating anti-idiotype antibodies.

xx SQ Sequence 142 AA;

xx SQ Query Match 100.0%; Score 655; DB 16; Length 142;

xx DB Best Local Similarity 100.0%; Pred. No. 8.4e-53; Mismatches 0; Indels 0; Gaps 0; Matches 123; Conservative 0;

Qy 1 QVQLVQSGAEVKPGASKVSKASGNIKDTYIHWVQAPGQLEWGRIDPANGTYK 60

Db 20 QVQLVQSGAEVKPGASKVSKASGNIKDTYIHWVQAPGQLEWGRIDPANGTYK 79

Qy 61 DPKFQGRVITTAQTSASATAYMELSSLRSQEDAVYTCARSGTYYKGYAMDYWGQGTVY 120

Db 80 DPKFQGRVITTAQTSASATAYMELSSLRSQEDAVYTCARSGTYYKGYAMDYWGQGTVY 139

Qy 121 VSS 123

Db 140 VSS 142

xx RESULT 3
AAW22428

xx ID AAW22428 standard; Protein: 142 AA.

xx AC AAW22428;

xx DR 09-DEC-1997 (first entry)

xx DE Humanised alpha-4 integrin antibody 21.6 VL version Ha.

xx KW Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;

kw asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;

kw metastasis; inflammatory bowel disease; rheumatoid arthritis;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:10:55 ; Search time 15.903 Seconds
(without alignments)

327.248 Million cell updates/sec

Title: US-09-155-739-11
Perfect score: 655
Sequence: 1 QVQLVQSGAEVKPGASVKV NYGYAMDYWGQGTIVTVSS 123

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

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3: /cgn2_6/podata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/podata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/podata/1/iaa/PCT05.COMB.pep:*

6: /cgn2_6/podata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1
US-09-155-739-11
; Sequence 11, Application US/08561521
; Patent No. 5840299

GENERAL INFORMATION:

APPLICANT: Bendig, Mary M.

Leger, Olivier J.

Sandana, Jose

Jones, S. Tarran

TITLE OF INVENTION: Humanized Antibodies Against Leukocyte

TITLE OF INVENTION: Adhesion Molecule VIIA 4

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/561,521

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/186,269A

FILING DATE: 25-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William L.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 15270-14

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-543-9600

TELEFAX: 415-543-5043

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 123 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-561-521-11

Query Match Score 655: DB 2; Length 123;

Best Local Similarity 100.0%; Pred. No. 2.7e-58;

Matches 123; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

ALIGNMENTS

28 486 74.2 140 3 US-08-836-561-63
29 486 74.2 140 4 US-09-422-63
30 484.5 74.0 135 1 US-08-137-117D-112
31 484.5 74.0 135 2 US-08-436-717-112
32 484.5 74.0 139 1 US-08-253-877C-19
33 484.5 74.0 139 2 US-08-452-164A-19
34 484.5 74.0 139 3 US-08-603-024-18
35 484.5 74.0 139 4 US-08-450-809-14
36 481 73.4 121 1 US-08-202-047-13
37 481 73.4 121 3 US-08-964-690-23
38 480.5 73.4 124 4 US-09-301-593-16
39 480.5 73.4 124 4 US-09-438-954-4
40 475 72.5 119 3 US-08-836-561-74
41 474 72.4 140 3 US-08-482-882-53
42 473 72.2 123 1 US-08-483-389-53
44 473 72.2 123 2 US-08-487-113D-53
45 473 72.2 123 2 US-08-487-113D-53

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1	655	100.0	123	2	US-08-561-521-11		Sequence 11, Appl
2	655	100.0	123	5	PCT-US95-01219-1		Sequence 11, Appl
3	655	100.0	124	2	US-08-561-521-17		Sequence 17, Appl
4	655	100.0	142	5	PCT-US95-01219-17		Sequence 17, Appl
5	552	84.3	123	2	US-08-561-521-9		Sequence 9, Appl
6	552	84.3	123	5	PCT-US95-01219-9		Sequence 9, Appl
7	544	83.1	140	2	US-08-561-521-4		Sequence 4, Appl
8	544	83.1	140	5	PCT-US95-01219-4		Sequence 4, Appl
9	523.5	79.9	120	4	US-08-871-488A-19		Sequence 19, Appl
10	523	79.8	117	3	US-08-646-265A-132		Sequence 12, Appl
11	523	79.8	116	3	US-08-646-265A-19		Sequence 99, Appl
12	523	79.8	269	3	US-08-646-265A-109		Sequence 106, Appl
13	515	78.6	119	2	US-08-561-521-13		Sequence 13, Appl
14	515	78.6	119	5	PCT-US95-01219-13		Sequence 13, Appl
15	512	78.2	119	2	US-08-561-521-12		Sequence 12, Appl
16	512	78.2	119	5	PCT-US95-01219-12		Sequence 12, Appl
17	505	77.1	125	2	US-08-561-521-44		Sequence 44, Appl
18	505	77.1	125	5	PCT-US95-01219-44		Sequence 44, Appl
19	495	75.6	119	2	US-08-561-521-10		Sequence 10, Appl
20	495	75.6	119	5	PCT-US95-01219-10		Sequence 10, Appl
21	492	74.7	117	2	US-08-290-592E-17		Sequence 17, Appl
22	492	74.7	117	5	PCT-US95-10053-14		Sequence 17, Appl
23	492	75.1	117	5	PCT-US96-09448-17		Sequence 17, Appl
24	492	75.1	119	4	US-09-438-954-41		Sequence 41, Appl
25	491.5	75.0	118	2	US-08-232-081B-8		Sequence 8, Appl
26	489	74.7	120	4	US-09-025-769B-59		Sequence 36, Appl
27	489.5	74.7	120	4	US-09-025-769B-59		Sequence 59, Appl

Db 121 VSS 123

Db 121 VSS 123

RESULT 2
 PCT-US95-01219-11
 Sequence 11, Application PC/TUS9501219
 GENERAL INFORMATION:
 APPLICANT: Bendig, Mary M.
 APPLICANT: Leger, Olivier J.
 APPLICANT: Salданha, Jose
 APPLICANT: Jones, S. Tarran
 TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khoure and Crew
 STREET: One Market Plaza, Stewart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/TUS95/01219
 FILING DATE: 25-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/186,269
 FILING DATE: 25-JAN-1995
 INFORMATION FOR SEQ ID NO: 11:
 LENGTH: 123 amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US95-01219-11
 Query Match 100.0%; Score 655; DB 5; Length 123;
 Best Local Similarity 100.0%; Pred. NO. 2.7e-58;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CYQLQSGAEVKPGASVKSCASGNFKDDYIHWYRQAPQRLEWMGRIDPANGYTKY 60
 Db 1 CYQLQSGAEVKPGASVKSCASGNFKDDYIHWYRQAPQRLEWMGRIDPANGYTKY 60
 Db 121 VSS 123

RESULT 3
 US-08-561-521-17
 Sequence 17, Application US/08561521
 GENERAL INFORMATION:
 APPLICANT: Bendig, Mary M.
 APPLICANT: Leger, Olivier J.
 APPLICANT: Salданha, Jose
 APPLICANT: Jones, S. Tarran
 TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khoure and Crew
 STREET: One Market Plaza, Stewart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/561,521
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/186,269A
 FILING DATE: 25-JAN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William L.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 15270-14
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-541-9600
 TELEFAX: 415-541-5043
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 142 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-561-521-17
 Query Match 100.0%; Score 655; DB 2; Length 142;
 Best Local Similarity 100.0%; Pred. NO. 3.2e-58;
 Matches 123; Conservative 0; Mismatches 0; Indels 0
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 Qy 61 DPKFQGRVTTADTSASTAYMELSSRLSETAVYCARREGYIYNTGYAM
 Db 80 DPKFQGRVTTADTSASTAYMELSSRLSETAVYCARREGYIYNTGYAM
 RESULT 4
 PCT-US95-01219-17
 Sequence 17, Application PC/TUS9501219
 GENERAL INFORMATION:
 APPLICANT: Bendig, Mary M.
 APPLICANT: Leger, Olivier J.
 APPLICANT: Salданha, Jose
 APPLICANT: Jones, S. Tarran
 TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Khoure and Crew
 STREET: One Market Plaza, Stewart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/561,521
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/186,269
 FILING DATE: 25-JAN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William L.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 15270-14
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-541-9600
 TELEFAX: 415-541-5043
 INFORMATION FOR SEQ ID NO: 11:
 LENGTH: 123 amino acids
 SEQUENCE CHARACTERISTICS:
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US95-01219-11
 Query Match 100.0%; Score 655; DB 5; Length 123;
 Best Local Similarity 100.0%; Pred. NO. 2.7e-58;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CYQLQSGAEVKPGASVKSCASGNFKDDYIHWYRQAPQRLEWMGRIDPANGYTKY 60
 Db 1 CYQLQSGAEVKPGASVKSCASGNFKDDYIHWYRQAPQRLEWMGRIDPANGYTKY 60
 Db 121 VSS 123
 Qy 1 CYQLQSGAEVKPGASVKSCASGNFKDDYIHWYRQAPQRLEWMGRIDPANGYTKY 60
 Db 61 DPKFQGRVTTADTSASTAYMELSSRLSETAVYCARREGYIYNTGYAM
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 Db 140 VSS 142
 Qy 121 VSS 123
 Db 80 DPKFQGRVTTADTSASTAYMELSSRLSETAVYCARREGYIYNTGYAM
 Db 121 VSS 123

Gencore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 7, 2003, 09:18:36 ; Search time 31.0606 Seconds
(without alignments)
626.523 Million cell updates/sec

Title: US-09-155-739-11
Perfect score: 655
Sequence: 1 QVQLVQSGAEVKKPGASVKG.....NYGYAMDYWGQGTLYVSS 123

Scoring table: BL05UM62
Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

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5: /cgn2_6/pctodata/1/pubpaa/us07_new_pub.pep:*

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17: /cgn2_6/pctodata/1/pubpaa/us60_new_pub.pep:*

18: /cgn2_6/pctodata/1/pubpaa/us60_pubcomb.pep:*

ALIGNMENTS

RESULT 1
US-10-056-794-19
Sequence 19, Application US/10056794
; Publication No. US20030119078A1
; GENERAL INFORMATION:
; APPLICANT: Graves, Scott S.
; Reno, John M.
; Mallett, Robert W.
; Hylarides, Mark D.
; Searle, Stephen M.J.
; Henry, Andrew H.
; Pedersen, Jan T.
; REES, Anthony R.

TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT BIND TO THE ANTIGEN BOUND BY ANTIBODY NR-LU-13 AND THEIR USE IN PRETARGETING METHODS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patient Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/056,794
FILING DATE: 24-Jan-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey Ph.D., Richard G.
REGISTRATION NUMBER: 312,629
REFERENCE/DOCKET NUMBER: 690022.527C2
TELECOMMUNICATION INFORMATION:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	523.5	79.9	120	15	US-10-056-794-19
2	523.5	79.9	431	12	US-10-056-794-14
3	523.5	79.9	431	15	US-10-013-173-4
4	523.5	79.9	431	15	US-10-150-172-4
5	523	79.8	117	11	US-09-749-873-132
6	523	79.8	136	11	US-09-749-873-99
7	523	79.8	269	11	US-09-749-873-119
8	492	75.1	117	10	US-09-158-120A-17
9	492	75.1	119	15	US-10-233-396-41
10	491.5	75.0	245	11	US-09-880-748-1896
11	486	74.2	140	15	US-10-283-249-63
12	485.5	74.1	120	14	US-10-025-387-2
13	485.5	74.1	120	15	US-10-125-687-2
14	484	73.9	180	9	US-09-148-960-6
15	480.5	73.4	124	12	US-10-159-006-16

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 19:

US-10-056-794-19

Query Match 79.9%; Score 523.5; DB 15; Length 120;

Best Local Similarity 82.9%; Pred. No. 1.6e-45; Matches 102; Conservative 8; Mismatches 10; Indels 3; Gaps 1;

SEQ ID NO: 19

QY 1 QVQLVQSGAEVKKPGASVSKASFGNFKDYLHWRQAPQRLWGRIDPANGTYK 60

DB 1 QVQLVQSGAEVKKPGASVSKASFGNFKDYLHWRQAPQGLQGMGRIDPANGTYK 60

QY 61 DPKFQGRVTTADTSASATAYMELSLRSRDTAVYCAEGTYGNVYAMDYWGQTLV 120

DB 61 DLSFQGRVTTADTSINTAYMELSLRSRDTAVYCSREVL--TGTWSDLYWGQTLV 117

QY 121 VSS 123

DB 118 VSS 120

RESULT 2

US-10-244-821-4

Sequence 4, Application US/10244821

Publication No. US20030143233A1

GENERAL INFORMATION:

APPLICANT: Goshorn, Stephen Charles

APPLICANT: Graves, Scott Stoll

APPLICANT: Schultz, Joanne Elaine

APPLICANT: Sanders, James Allen

APPLICANT: Reno, John M.

APPLICANT: Dearstyne, Erica A.

TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND

METHODS OF USE THEREOF

FILE REFERENCE: 690022.547C3

CURRENT FILING DATE: 2002-09-16

NUMBER OF SEQ ID NOS: 92

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 4

LENGTH: 431

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Predicted amino acid sequence for hUNR-LU-10

OTHER INFORMATION: single chain antibody-genomic streptavidin fusion.

US-10-244-821-4

Query Match 79.9%; Score 523.5; DB 12; Length 431;

Best Local Similarity 82.9%; Pred. No. 7e-45; Matches 102; Conservative 8; Mismatches 10; Indels 3; Gaps 1;

SEQ ID NO: 4

QY 1 QVQLVQSGAEVKKPGASVSKASFGNFKDYLHWRQAPQRLWGRIDPANGTYK 60

DB 148 QVQLVQSGAEVKKPGASVSKASFGNFKDYLHWRQAPQGLQGMGRIDPANGTYK 207

QY 61 DPKFQGRVTTADTSASATAYMELSLRSRDTAVYCAEGTYGNVYAMDYWGQTLV 120

DB 208 DLSFQGRVTTADTSINTAYMELSLRSRDTAVYCSREVL--TGTWSDLYWGQTLV 264

QY 121 VSS 123

DB 265 VSS 267

RESULT 3

US-10-013-173-4

Sequence 4, Application US/10013173

Publication No. US2003005977A1

GENERAL INFORMATION:

APPLICANT: Goshorn, Stephen C.

APPLICANT: Graves, Scott Stoll

APPLICANT: Schultz, Joanne Elaine

APPLICANT: Sanders, James A.

APPLICANT: Reno, John M.

TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND

METHODS OF USE THEREOF

FILE REFERENCE: 690022.547C1

CURRENT FILING DATE: 2001-12-07

NUMBER OF SEQ ID NOS: 69

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 4

LENGTH: 431

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Predicted amino acid sequence for hUNR-LU-10

OTHER INFORMATION: single chain antibody-genomic streptavidin fusion.

US-10-150-762-4

Query Match 79.9%; Score 523.5; DB 15; Length 431;

A; Reference number: S07453; MUID:83058021; PMID:6815271

A; Molecule type: protein

A; Residues: 1-43 <GR>

C; Superfamily: immunoglobulin V region; immunoglobulin

C; Keywords: heterotetramer; immunoglobulin

F; 15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.3%; Score 477; DB 2; Length 120; Best Local Similarity 75.6%; Pred. No. 8e-36; Matches 93; Conservative 11; Mismatches 15; Indels 4; Gaps 1;

Qy 1 QYQLVQSGAEVKKPGASVVKVSCKASGFNIKDTYIHWVROAPGQRLEWMGRIDPANGTYK 60

Db 1 EVQLQSGAELVKKPGASVVKVSCKASGFNIKDTYIHWVROAPGQRLEWMGRIDPANGTYK 60

Qy 61 DPKFQGRVITADTSASTAYMELSSRSEDTAVVYCARASYGTYGTYAMDYWGQGTLYT 120

Db 61 DPKFQGRVITADTSNTAYLQLSSRSEDTAVVYCARASYGTYGTYAMDYWGQGTLYT 116

Qy 121 VSS 123

Db 117 VSS 119

RESULT 3
S36265 Ig heavy chain V region (clone alpha-muc1-1) - human (fragment)
C; Species: Homo sapiens (man)
C; Date: 03-Feb-1994 *sequence_revision 03-Feb-1994 *text_change 23-Jul-1999
C; Accession: S36265
R; Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J. EMBO J. 12: 725-734, 1993
A; Title: Human anti-self antibodies with high specificity from phage display libraries.
A; Reference number: S36265
A; Status: preliminary; nucleic acid sequence not shown

A; Molecule type: mRNA

A; Residues: 1-18 <GR>

C; Superfamily: immunoglobulin V region; immunoglobulin

F; 15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.3%; Score 473.5; DB 2; Length 118; Best Local Similarity 76.2%; Pred. No. 1.6e-35; Matches 96; Conservative 6; Mismatches 13; Indels 11; Gaps 2;

Qy 1 QYQLVQSGAEVKKPGASVVKVSCKASGFNIKDTYIHWVROAPGQRLEWMGRIDPANGTYK 60

Db 1 QYQLVQSGAEVKKPGASVVKVSCKASGFNIKDTYIHWVROAPGQRLEWMGRIDPANGTYK 60

Qy 61 DPKFQGRVITADTSASTAYMELSSRSEDTAVVYCARASYGTYGTYAMDYWGQGT 117

Db 61 DPKFQGRVITADTSASTAYMELSSRSEDTAVVYCARDFLSGY-----LDWGQGT 112

Qy 118 LYTVSS 123

Db 113 LYTVSS 118

A; Molecule type: mRNA

A; Residues: 1-13 <KIP>

C; Superfamily: immunoglobulin V region; immunoglobulin homology

C; Keywords: heterotetramer; immunoglobulin

F; 15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.0%; Score 477; DB 2; Length 120; Best Local Similarity 75.6%; Pred. No. 8e-36; Matches 93; Conservative 11; Mismatches 15; Indels 4; Gaps 0;

Qy 1 QYQLVQSGAEVKKPGASVVKVSCKASGFNIKDTYIHWVROAPGQRLEWMGRIDPANGTYK 60

Db 1 QYQLVQSGAEVKKPGASVVKVSCKASGFNIKDTYIHWVROAPGQRLEWMGRIDPANGTYK 60

Qy 61 DPKFQGRVITADTSASTAYMELSSRSEDTAVVYCARASYGTYGTYAMDYWGQGTLYT 120

Db 61 DPKFQGRVITADTSNTAYLQLSSRSEDTAVVYCARASYGTYGTYAMDYWGQGTLYT 120

Qy 121 VSS 123

Db 121 VSS 123

RESULT 5
A32483 Ig heavy chain V region - human (fragment)

C; Species: Homo sapiens (man)

C; Date: 12-Oct-1989 *sequence_revision 12-Oct-1989 *text_change 16-Aug-1996

C; Accession: A32483

R; Larrick, J.W.; Danielsson, L.; Brenner, C.A.; Abramson, M.; Fry, K.E.; Borrebaek

Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989

A; Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells

A; Reference number: A32483; MUID:89213586; PMID:2499327

A; Accession: A32483

A; Status: preliminary

A; Molecule type: mRNA

A; Residues: 1-142 <LAR>

A; Cross-references: GB: M26463

C; Superfamily: immunoglobulin V region; immunoglobulin homology

F; 25-108/Domain: immunoglobulin homology <IMM>

Query Match 71.3%; Score 467; DB 2; Length 142; Best Local Similarity 73.2%; Pred. No. 7.5e-35; Matches 93; Conservative 8; Mismatches 22; Indels 4; Gaps 1;

Qy 1 QYQLVQSGAEVKKPGASVVKVSCKASGFNIKDTYIHWVROAPGQRLEWMGRIDPANGTYK 60

Db 11 QYQLVQSGAEVKKPGASVVKVSCKASGFNIKDTYIHWVROAPGQRLEWMGRIDPANGTYK 70

Qy 61 DPKFQGRVITADTSASTAYMELSSRSEDTAVVYCARASYGTYGTYAMDYWGQGT 116

Db 71 DPKFQGRVITADTSNTAYLQLSSRSEDTAVVYCARASYGTYGTYAMDYWGQGT 130

Qy 117 TLTVSS 123

Db 131 TLTVSS 137

RESULT 6
S17586 Ig heavy chain V region (E8) - mouse (fragment)

C; Species: Mus musculus (house mouse)

C; Date: 22-Nov-1993 *sequence_revision 26-May-1995 *text_change 21-Jan-2000

C; Accession: S17586

R; Mylvaganam, S.E.; Paterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff, E.D.

J. Mol. Biol. 221, 455-462, 1991

A; Title: Biochemical implications from the variable gene sequences of an anti-cytochr

forms.

A; Reference number: S17586; MUID:92015240; PMID:1656053

A; Status: preliminary

A; Molecule type: mRNA

A; Reference number: A33548

A; Molecule type: protein

A; Residues: 1-18 <GR>

C; Superfamily: immunoglobulin V region; immunoglobulin

C; Keywords: heterotetramer; immunoglobulin

F; 15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.0%; Score 477; DB 2; Length 120; Best Local Similarity 75.6%; Pred. No. 8e-36; Matches 93; Conservative 11; Mismatches 15; Indels 4; Gaps 0;

Qy 1 QYQLVQSGAEVKKPGASVVKVSCKASGFNIKDTYIHWVROAPGQRLEWMGRIDPANGTYK 60

Db 1 QYQLVQSGAEVKKPGASVVKVSCKASGFNIKDTYIHWVROAPGQRLEWMGRIDPANGTYK 60

Qy 61 DPKFQGRVITADTSASTAYMELSSRSEDTAVVYCARASYGTYGTYAMDYWGQGT 117

Db 61 DPKFQGRVITADTSASTAYMELSSRSEDTAVVYCARDFLSGY-----LDWGQGT 112

Qy 118 LYTVSS 123

Db 113 LYTVSS 118

Scoring table:	BLOSUM62				BLOSUM62				
Scanned:	Gapop 10.0 , Gapext 0.5				Searches:	Gapop 10.0 , Gapext 0.5 residues			
Total number of hits satisfying chosen parameters:					127863				
Minimum DB seq length:	0	Minimum DB seq length:	2000000000	Post-processing:	Minimum Match 0%	Maximum Match 100%	Listing first 45 summaries		
Database :	SwissProt_41;*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
Result No.	Score	Query	Match	Length	DB	ID	Description		
1	427.5	B6YD62	65.3	147	1	HV1C_HUMAN	P01744	homo sapien	
2	409	1QWLYQSGAEEVKPGASVKV	62.4	120	1	HV03_MOUSE	P01747	mus musculus	
3	408.5	1QWLYQSGAEEVKPGASVKV	62.4	139	1	HV07_MOUSE	P01751	mus musculus	
4	405	1QWLYQSGAEEVKPGASVKV	61.8	117	1	HV1B_HUMAN	P01743	homo sapien	
5	399	1QWLYQSGAEEVKPGASVKV	60.9	140	1	HV02_MOUSE	P01746	mus musculus	
6	396	1QWLYQSGAEEVKPGASVKV	60.5	117	1	HV1G_HUMAN	P023083	homo sapien	
7	390	1QWLYQSGAEEVKPGASVKV	59.5	117	1	HV1A_HUMAN	P01742	homo sapien	
8	378	1QWLYQSGAEEVKPGASVKV	57.7	117	1	HV13_MOUSE	P01757	mus musculus	
9	375.5	1QWLYQSGAEEVKPGASVKV	57.3	118	1	HV51_MOUSE	P06330	mus musculus	
10	373	1QWLYQSGAEEVKPGASVKV	56.9	117	1	HV12_MOUSE	P01756	mus musculus	
11	371.5	1QWLYQSGAEEVKPGASVKV	56.7	137	1	HV11_MOUSE	P01755	mus musculus	
12	369	1QWLYQSGAEEVKPGASVKV	56.3	138	1	HV48_MOUSE	P03980	mus musculus	
13	364.5	1QWLYQSGAEEVKPGASVKV	55.6	120	1	HV50_MOUSE	P06329	mus musculus	
14	360	1QWLYQSGAEEVKPGASVKV	55.0	121	1	HV01_MOUSE	P01748	mus musculus	
15	360	1QWLYQSGAEEVKPGASVKV	55.0	136	1	HV15_MOUSE	P01759	mus musculus	
16	355	1QWLYQSGAEEVKPGASVKV	54.2	125	1	HV1F_HUMAN	P06326	homo sapien	
17	349.5	1QWLYQSGAEEVKPGASVKV	53.4	120	1	HV1H_HUMAN	P080421	homo sapien	
18	349	1QWLYQSGAEEVKPGASVKV	53.3	117	1	HV09_MOUSE	P01753	mus musculus	
19	344.5	1QWLYQSGAEEVKPGASVKV	52.6	114	1	HV00_MOUSE	P01741	mus musculus	
20	338	1QWLYQSGAEEVKPGASVKV	51.6	117	1	HV04_MOUSE	P01748	mus musculus	
21	336	1QWLYQSGAEEVKPGASVKV	51.3	117	1	HV06_MOUSE	P01750	mus musculus	
22	333.5	1QWLYQSGAEEVKPGASVKV	50.9	136	1	HV16_MOUSE	P01783	mus musculus	
23	333	1QWLYQSGAEEVKPGASVKV	50.8	117	1	HV10_MOUSE	P01754	mus musculus	
24	330.5	1QWLYQSGAEEVKPGASVKV	50.5	124	1	HV1E_HUMAN	P01761	homo sapien	
25	329	1QWLYQSGAEEVKPGASVKV	50.2	117	1	HV14_MOUSE	P01758	mus musculus	
26	329	1QWLYQSGAEEVKPGASVKV	50.2	117	1	HV49_MOUSE	P06328	mus musculus	
27	326	1QWLYQSGAEEVKPGASVKV	49.8	117	1	HV52_MOUSE	P06327	mus musculus	
28	326	1QWLYQSGAEEVKPGASVKV	49.8	123	1	HV24_MOUSE	P01793	mus musculus	
29	325.5	1QWLYQSGAEEVKPGASVKV	49.7	119	1	HV37_MOUSE	P01807	mus musculus	
30	325.5	1QWLYQSGAEEVKPGASVKV	49.7	124	1	HV1D_HUMAN	P01760	homo sapien	
31	324.5	1QWLYQSGAEEVKPGASVKV	49.5	119	1	HV40_MOUSE	P01808	mus musculus	
32	323.5	1QWLYQSGAEEVKPGASVKV	49.4	119	1	HV36_HUMAN	P01810	mus musculus	
33	320.5	1QWLYQSGAEEVKPGASVKV	48.9	122	1	HV35_HUMAN	P01768	homo sapien	

ALIGNMENTS

RESULT 1	HVIC_HUMAN				STANDARD				PRT;	147 AA.
ID	HVIC_HUMAN				AC	P01744;				
AC	P01744;				DT	21-JUL-1986	(Rel. 01, Created)			
					DT	16-OCT-2001	(Rel. 40, Last sequence update)			
					DT	15-SEP-2003	(Rel. 42, Last annotation update)			
DE					DE	IG heavy chain V-I region ND precursor (fragments).				
OS					OS	Homo sapiens (Human)				
OC					OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
CC					CC	NCBI_Taxid=9606;				
RN					RN	[1]				
RP					RP	SEQUENCE FROM N.A.				
RA					RA	SEQUENCEID=8306534; PubMed=681656;				
RA					RA	Keenan J.H., Molsgaard H.V., Houghton M., Derbyshire R.B., Viney J., Bell L.O., Gould H.J.;				
RA					RA	*Cloning and sequence determination of the gene for the human immunoglobulin epsilon chain expressed in a myeloma cell line.";				
RT					RT	Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).				
RL					RL	[12]				
RP					RP	SEQUENCE OF 20-147.				
RA					RA	Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.,				
RL					RL	(IN) Bach M.K. (eds.);				
RL					RL	Immediate hypersensitivity: modern concepts and developments, pp.1-36.				
RL					RL	Marcel Dekker, New York (1978).				
CC					CC	-1- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.				
CC					CC	-1- SIMILARITY: Contains 1 immunoglobulin-like domain.				
DR					DR	HSSP: P01789; 1IMCP.				
DR					DR	GO; GO:0005576; C:extracellular; NAS.				
DR					DR	GO; GO:0003823; F:antigen binding activity; NAS.				
DR					DR	GO; GO:0006955; F:immune response; NAS.				
DR					DR	InterPro: IPR007110; Ig-like.				
DR					DR	InterPro: IPR003006; Ig_MHC.				
DR					DR	InterPro: IPR03596; Ig_V.				
PFam:	P060047; ig; 1.				PFam:	PF00047; ig; 1.				
SMART:	SM00406; ig; 1.				SMART:	SM00406; ig; 1.				
PS50835:	PS50835; Ig_LIKE; 1.				PS50835:	PS50835; Ig_LIKE; 1.				
KW					KW	Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.				
FT					FT	SIGNAL	1	19		
FT					FT	IG	19	147	IG HEAVY CHAIN V-I REGION ND.	
FT					FT	DOMAIN	20	131	IG-1IKE.	
FT					FT	MOD_RES	20	20	PYRROLIDONE CARBOXYLIC ACID.	
FT					FT	DISULFID	41	115		
FT					FT	CONFFLICT	21	21	T -> V (IN REF. 2).	
FT					FT	CONFFLICT	53	54	IH -> HI (IN REF. 2).	
FT					FT	CONFFLICT	67	68	VG -> GV (IN REF. 2).	
FT					FT	CONFFLICT	125	125	MISSING (IN REF. 2).	
FT					FT	NON_TER	147	147		
SQ					SQ	SEQUENCE	147 AA.	16491 MW;	948F9F72A5366C20 CRC64;	

Query Match 65.3%; Score 427.5; DB 1; Length 147;
 Best Local Similarity 64.1%; Pred. No. 1.1e-36;
 Matches 82; Conservative 16; Mismatches 25; Indels 5; Gaps 1;

1 QVQLVSGAELVKPGASVKVSCKASGFNIKDTYIHWVROAPGORLEWGRIDPANGTYK 60
 20 QTOQVSGAELVKPGASVKVSCKASGFNIKDTYIHWVROAPGHLEWGRINPNSGTYN 79

QY 61 DPKFQGRVTITADTSASTAYMELSSRSEDTAYYCAR---EGYTYGNYGYAMDWGQ 115
 DB 80 APRFQGRVTMTRDASSTAYMDRSLSRSDDSAVYCAKSDDPFWSDYNTEDSYTLDWQ 139

QY 116 GTLVYSS 123
 DB 140 GTRVIVSS 147

RESULT 2
 HV03_MOUSE STANDARD: PRT; 120 AA.

ID HV03_MOUSE STANDARD: PRT; 120 AA.
 AC P01747;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DB Ig heavy chain V region 36-65.
 OS Mus musculus (Mouse).
 Euksaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83131846; PubMed=6186498;
 RA Siekavitz M., Geftter M.L., Brodeur P., Riblet R.,
 RA Marshak-Rothstein A.;
 RT "The genetic basis of antibody production: the dominant anti-arsenite idiotypic response of the strain A mouse.";
 RL Eur. J. Immunol. 12:1023-1032(1982).
 CC 1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J SEGMENT, JH2.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR HSSP_P01789; MCP.
 DR InterPro; IPR07110; Ig-like.
 DR InterPro; IPR03006; Ig_MHC.
 DR InterPro; IPR03596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00106; IgV; 1.
 DR SMART; PS50835; Ig_LIKE; 1.
 KW Immunoglobulin V region; Hybirdoma.
 FT DOMAIN 1 111 Ig-LIKE.
 FT DOMAIN 120 120 NON_TER MW: FFO4EA167B654AF CRC64;
 SQ SEQUENCE 120 AA; 13307 MW; 1B57DD4FD0C9F465 CRC64;

Query Match 62.4%; Score 409; DB 1; Length 139;
 Best Local Similarity 63.1%; Pred. No. 6.5e-35; Indels 2; Gaps 1;
 Matches 77; Conservative 18; Mismatches 25; Indels 25; Gaps 3; Gaps 1;

QY 2 VOLQVSGAELVKPGASVKVSCKASGFNIKDTYIHWVROAPGQRLEWGRIDPANGTYK 61
 DB 1 VOLQVSGAELVKPGASVKVSCKASGFNIKDTYIHWVROAPGQRLEWGRIDPANGTYK 60

QY 62 PKFQGRVTITADTSASTAYMELSSRSEDTAYYCARREGYGNNGYAMDWGQTLTV 121
 DB 61 EKFKGKTTLTVDKSSSTAYMQLRSLSEDSAVYCAKSDDPFWSDYNTEDSYTLDWQ 118

QY 122 SS 123
 DB 119 SS 120

RESULT 3
 HV07_MOUSE STANDARD: PRT; 139 AA.
 AC P01751; P01752;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE 19 heavy chain V region B1-8/186-2 precursor.
 OS Mus musculus (Mouse).
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAINC57BL/6;
 RX MEDLINE=81234548; PubMed=6788376;
 RA Bothwell A.L.M., Pastind M., Reth M., Imanishi-Kari T., Rajewsky K., Baltimore D.;
 RA RT *Heavy chain variable region contribution to the NpB family of antibodies: somatic mutation evident in a gamma 2a variable region.*;
 RL Cell 24:625-637(1981).
 CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPten (4-HYDROXY-3-NITROPHENYL)ACETYL (NpB ANTIBODIES).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and thus statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC EMBL; J00529; AAA38170; 1- .
 DR PIR; A90809; MHNS18.
 DR PDB; 1A6U; 27-MAY-98.
 DR PDB; 1A6W; 15-JUL-98.
 DR InterPro; IPR07110; Ig-like.
 DR InterPro; IPR03006; Ig_MHC.
 DR InterPro; IPR03596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00106; IgV; 1.
 DR SMART; PS50835; Ig_LIKE; 1.
 KW Immunoglobulin V region; Signal; 3D-structure.
 FT SIGNAL 1 19
 FT CHAIN 20 139 Ig HEAVY CHAIN V REGION B1-8/186-2.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 DR DISULFID 41 17 DR SEGMENT-3.
 FT DOMAIN 118 124 DR SEGMENT-4.
 FT DOMAIN 125 139 JH2 SEGMENT.
 FT DISULFID 41 17 BY SIMILARITY.
 FT NON_TER 139 139 SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match 62.4%; Score 408.5; DB 1; Length 139;
 Best Local Similarity 62.6%; Pred. No. 8.6e-35; Indels 25; Gaps 3; Gaps 1;
 Matches 77; Conservative 18; Mismatches 25; Indels 3; Gaps 1;

QY 1 VOLQVSGAELVKPGASVKVSCKASGFNIKDTYIHWVROAPGQRLEWGRIDPANGTYK 60
 DB 20 VOLQVSGAELVKPGASVKVSCKASGFNIKDTYIHWVROAPGQRLEWGRIDPANGTYK 79

QY 61 DPKFQGRVTITADTSASTAYMELSSRSEDTAYYCARREGYGNNGYAMDWGQTLTV 120
 DB 80 NEKFKGKTTLTVDKSSSTAYMQLRSLSEDSAVYCAKSDDPFWSDYNTEDSYTLDWQ 116

QY 121 VSS 123
 DB 137 VSS 139

RESULT 4
 HV07_HUMAN STANDARD: PRT; 117 AA.
 AC P01743;
 DT 21-JUL-1986 (Rel. 01, Created)

1 EVQLVESGAEVKKPGASVKVSCKASGYTFSSYYMWVQAPGQLEWANGIINPSGGTSY 60
 61 DPKFQGRVTADTSASTAYMELSSRSEDATAVYCAREYYGNYGYVAM-----DY 112
 |||||: ||| ||| ||| ||| ||| ||| ||| : ||| :
 61 AOKFQGRVTADTSASTAYMELSSRSEDATAVYCAREYYGNYGYVAM-----GLYVVVPAAFSFRDY 113
 ||| :
 DB 113 WQGTLYVSS 123
 ||| :
 QY 114 WQGTLYVSS 124
 ||| :
 DB 114 WQGTLYVSS 124

RESULT 2
 Q96QSO ID Q96QSO; PRELIMINARY; PRT; 159 AA.
 AC Q96QSO;
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 Putative matrix cell adhesion molecule-2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tjilson M.D.;
 RT Homo sapiens putative microfibrillar protein with Ig-like domain 3
 RT mRNA (Matrix Cell Adhesion Molecule-3, Mat-SAM 3);
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR AY039025; AAK82649; 1.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR03006; Ig_MHC.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; Ig_LIKE; 1.
 SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;
 ||| :
 Query Match 67.38; Score 440.5; DB 4; Length 159;
 Best Local Similarity 64.9%; pred. No. 6.4e-39;
 Matches 87; Conservative 13; Mismatches 19; Indels 15; Gaps 2;
 PRT; 159 AA.

Q96QSO ID Q96QSO; PRELIMINARY; PRT; 159 AA.
 AC Q96QSO;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Anti-myosin immunoglobulin heavy chain variable region
 DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RX MEDLINE-2044942; PubMed-10392488;
 RA Liao L., Cunningham M.W., Diamond B.;
 RT "T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin."
 RT Infec. Immun. 68:5803-5808(2000).
 DR EMBL; AF206021; AAF69319.1; --.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; Ig_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11944 MW; DPE615FE6CD4EDE CRC64;

Query Match 66.0%; Score 432; DB 11; Length 109;
 Best Local Similarity 68.7%; Pred. No. 3.2e-38;
 Matches 79; Conservative 15; Mismatches 15; Indels 6; Gaps 1;

Q96QSO ID Q96QSO; PRELIMINARY; PRT; 159 AA.
 AC Q96QSO;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Similar to RIKEN cDNA 1810060003 gene.
 OS Mus musculus (Mouse).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBITAXID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 DR Submitted (FBB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC003878; AAH03878; 1.
 DR HSSP; P018442; 7FAB.

XX	PN	W09519790-A1.	OS	Homo sapiens.
XX	PD	27-JUL-1995.	XX	Key
XX	PF	95W0-US01219.	PH	Peptide
XX	PF	25-JAN-1995;	FT	Region
XX	PR	25-JAN-1994;	FT	Region
XX	PA	(ATHENA) ATHENA NEUROSCIENCES INC.	FT	Region
XX	PI	Jones TS, Leger OJ, Saldanha J;	FT	Region
XX	DR	WPI; 1995-269276/35.	FT	Region
DR	N-PSDB;	AAQ99889.	FT	Region
XX	PT	New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating inflammatory disease.	FT	Region
XX	PS	Disclosure; Fig 1; 105pp; English.	FT	Region
XX	CC	The sequence represents the mouse antibody 21.6 light chain variable region directed against leukocyte adhesion molecule VLA-4. Cloned CC DNA sequences of mouse 21.6 VL and VH (see AAQ99892) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, CC L49, L58 and L69 in the human kappa LC VR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric antibodies are transferred into COS cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and to treat inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating anti-idiotype antibodies.	PN	W09519790-A1.
XX	SQ	Sequence 126 AA;	XX	PD 27-JUL-1995.
CC	Query Match	100.0%	XX	25-JAN-1995;
CC	Best Local Similarity	100.0%	PF	95W0-US01219.
Matches 126;	Conservative	0;	XX	25-JAN-1994;
Matches 126;	Mismatches	0;	PR	109..116
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Db	1	MRPSIQFLGLLFWLHGAGQCDIOMTQSPSSLSASLGSKVITCKTSQDINKYMANQHKP	(ATHENE) ATHENA NEUROSCIENCES INC.	/note= "framework region 1"
QY	61	GKRPRLLIHYTSALQPGIPSRSFSGSGRSRDSFVNISNLEPEDIATYYCLQYDNLWTFGGG	PI	/note= "framework region 2"
Db	61	GKRPRLLIHYTSALQPGIPSRSFSGSGRSRDSFVNISNLEPEDIATYYCLQYDNLWTFGGG	Bendig MM, Jones TS, Leger OJ, Saldanha J;	/note= "framework region 3"
QY	121	TKLETK 126	WPI	/note= "framework region 4"
Db	121	TKLEK 126	DR	WPI-269276/35.
XX	PS	Disclosure; Fig 10; 105pp; English.	DR	AAQ99893.
XX	CC	The sequence represents the human reshaped antibody 21.6 light chain variable region against leukocyte adhesion molecule VLA-4. Cloned cDNA sequences of mouse 21.6 VL (AAQ99889) and VH (AAQ99892) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized light chain, amino acids L45, L49, L58 and L69 in the human kappa LC VR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric antibodies are transferred into COS cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell and to treat inflammatory diseases such as multiple sclerosis. They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating anti-idiotype antibodies.	DR	AAQ99893.
XX	SQ	Sequence 126 AA;	XX	94US-0186269.
CC	Query Match	100.0%	XX	94US-0186269.
CC	Best Local Similarity	100.0%	PR	94US-0186269.
Matches 126;	Conservative	0;	PA	PA
Matches 126;	Mismatches	0;	XX	XX
QY	1	MRPSIQFLGLLFWLHGAGQCDIOMTQSPSSLSASLGSKVITCKTSQDINKYMANQHKP	XX	XX
Db	1	MRPSIQFLGLLFWLHGAGQCDIOMTQSPSSLSASLGSKVITCKTSQDINKYMANQHKP	XX	XX
QY	61	GKRPRLLIHYTSALQPGIPSRSFSGSGRSRDSFVNISNLEPEDIATYYCLQYDNLWTFGGG	XX	XX
Db	61	GKRPRLLIHYTSALQPGIPSRSFSGSGRSRDSFVNISNLEPEDIATYYCLQYDNLWTFGGG	XX	XX
RESULT 2			QY	1 MRPSIQFLGLLFWLHGAGQCDIOMTQSPSSLSASLGSKVITCKTSQDINKYMANQHKP
ID	AAR81332	standard; Protein; 126 AA.	Db	1 MRPSIQFLGLLFWLHGAGQCDIOMTQSPSSLSASLGSKVITCKTSQDINKYMANQHKP
XX	AC	AAR81332;	QY	61 GKRPRLLIHYTSALQPGIPSRSFSGSGRSRDSFVNISNLEPEDIATYYCLQYDNLWTFGGG
XX	DT	23-MAR-1996 (first entry)	Db	61 GKRPRLLIHYTSALQPGIPSRSFSGSGRSRDSFVNISNLEPEDIATYYCLQYDNLWTFGGG
DE	Human VLA-4 reshaped antibody 21.6 light chain variable region.	XX		
XX	KW	Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic; antibody engineering.		
XX				

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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:10:55 ; Search time 16.2909 Seconds
(without alignments)
327.248 Million cell updates/sec

Title: US-09-155-739-2

Perfect score: 680

Sequence: 1 MRPSIQFLGLLFWLHGAC YCLOQDNLWTFGGTKLEIK 126

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Parents AA:
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3: /cgn2_6/ptodata/1/iaa/6A_COMBO.pep:
4: /cgn2_6/ptodata/1/iaa/6B_COMBO.pep:
5: /cgn2_6/ptodata/1/iaa/PC05_COMBO.pep:
6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	680	100.0	126	2 US-08-561-521-15	Sequence 2, Appli
2	680	100.0	126	5 PCT-US95-01219-2	Sequence 15, Appli
3	680	100.0	126	5 PCT-US95-01219-15	Sequence 15, Appli
4	680	93.2	128	1 US-08-339-582-4	Sequence 4, Appli
5	659	83.7	106	2 US-08-561-521-5	Sequence 5, Appli
6	7	83.7	106	5 PCT-US95-01219-5	Sequence 5, Appli
7	569	83.7	106	5 PCT-US95-01219-7	Sequence 5, Appli
8	539	79.3	359	4 US-09-646-028-16	Sequence 16, Appli
9	539	79.3	361	4 US-09-646-028-13	Sequence 13, Appli
10	535	78.7	374	4 US-09-646-028-15	Sequence 15, Appli
11	510.5	75.1	107	2 US-08-880-366-22	Sequence 22, Appli
12	508	74.7	106	2 US-08-561-521-7	Sequence 7, Appli
13	508	74.7	106	5 PCT-US95-01219-7	Sequence 7, Appli
14	508	74.7	637	1 US-08-235-838-16	Sequence 16, Appli
15	508	74.7	637	2 US-08-465-738-16	Sequence 16, Appli
16	503	74.0	241	1 US-08-235-838-11	Sequence 11, Appli
17	503	74.0	241	2 US-08-465-473B-11	Sequence 11, Appli
18	501	73.7	355	3 US-08-875-811-57	Sequence 57, Appli
19	438.5	64.5	128	1 US-08-259-372-14	Sequence 14, Appli
20	438.5	64.5	128	1 US-08-468-671-14	Sequence 14, Appli
21	437.5	64.3	127	1 US-08-558-516-5	Sequence 5, Appli
22	437.5	64.3	127	3 US-08-348-548-4	Sequence 4, Appli
23	437.5	64.3	127	5 PCT-US95-15716-4	Sequence 4, Appli
24	437.5	64.3	131	1 US-08-236-520-2	Sequence 2, Appli
25	437.5	64.3	131	5 PCT-US95-05262-2	Sequence 2, Appli
26	435.0	64.0	134	4 US-09-740-002-24	Sequence 10, Appli
27	434.5	63.9	128	4 US-09-225-322B-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-09-155-521-2
; Sequence 2, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bending, Mary M.
; Leger, Olivier J.
; APPLICANT: Sardana, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; ADHESIN Molecule VII 4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9560
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-155-521-2
; Query Match Score 680; DB 2; Length 126;
; Best Local Similarity 100.0%; Pred. No. 2.le-59;
; Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GKRPLLHYTSALQGIPSPRSFGSGRDSYNSNLEPDIATYCLQYDNLWTFGGG 120
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 Db 61 GKRPLLHYTSALQGIPSPRSFGSGRDSYNSNLEPDIATYCLQYDNLWTFGGG 120

QY 121 TKLEIK 126
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 Db 121 TKLEIK 126

RESULT 2
 US-08-561-521-15
 ; Sequence 15, Application US/08561521
 ; Patent No. 5840399
 ; GENERAL INFORMATION:
 ; APPLICANT: Bendig, Mary M.
 ; APPLICANT: Leger, Olivier J.
 ; APPLICANT: Saldanha, Jose
 ; APPLICANT: Jones, S. Tarran
 ; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: One Market Plaza, Stewart Tower, Suite 2000
 ; CITY: San Francisco
 ; COUNTRY: USA
 ; ZIP: 94105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/01219
 ; FILING DATE: 25-JAN-1995
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/186,269
 ; FILING DATE: 25-JAN-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William L.
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 15270-14
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-543-9600
 ; TELEFAX: 415-543-5043
 ; INFORMATION FOR SEQ ID NO: 2:
 ; CLASSIFICATION: 42A
 ; PRIORITY APPLICATION DATA: US/08/186,269A
 ; APPLICATION NUMBER: US/08/186,269A
 ; FILING DATE: 25-JAN-1994
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/561,521
 ; FILING DATE:
 ; CLASSIFICATION: 42A
 ; PRIORITY APPLICATION DATA: US/08/186,269A
 ; APPLICATION NUMBER: US/08/186,269A
 ; FILING DATE: 25-JAN-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William L.
 ; REGISTRATION NUMBER: 30,223
 ; REFERENCE/DOCKET NUMBER: 15270-14
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-543-9600
 ; TELEFAX: 415-543-5043
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 126 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-561-521-15

Query Match 100.0%; Score 680; DB 2; Length 126;
 Best Local Similarity 100.0%; Pred. No. 2.1e-59; Indels 0; Gaps 0;
 Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GKRPLLHYTSALQGIPSPRSFGSGRDSYNSNLEPDIATYCLQYDNLWTFGGG 120
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QY 121 TKLEIK 126
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Db 121 TKLEIK 126

RESULT 3
 Sequence 2, Application PC/TUS9501219
 ; GENERAL INFORMATION:
 ; APPLICANT: Bendig, Mary M.
 ; APPLICANT: Leger, Olivier J.
 ; APPLICANT: Saldanha, Jose
 ; APPLICANT: Jones, S. Tarran
 ; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: One Market Plaza, Stewart Tower, Suite 2000
 ; CITY: San Francisco
 ; COUNTRY: USA
 ; STATE: California
 ; ZIP: 94105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/01219
 ; FILING DATE: 25-JAN-1995
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/186,269
 ; FILING DATE: 25-JAN-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William L.
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 126 amino acids
 ; REFERENCE/DOCKET NUMBER: 15270-14
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-543-9600
 ; TELEFAX: 415-543-5043
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 126 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US95-01219-2

Query Match 100.0%; Score 680; DB 5; Length 126;
 Best Local Similarity 100.0%; Pred. No. 2.1e-59; Indels 0; Gaps 0;
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QY 121 TKLEIK 126
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RESULT 4
 PCT-US95-01219-15
 ; Sequence 15, Application PC/TUS9501219
 ; GENERAL INFORMATION:
 ; APPLICANT: Bendig, Mary M.
 ; APPLICANT: Leger, Olivier J.
 ; APPLICANT: Saldanha, Jose
 ; APPLICANT: Jones, S. Tarran

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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:18:36 ; Search time 31.8182 Seconds
(without alignments)
626.523 Million cell updates/sec

Title: US-09-155-739-2
Perfect score: 680
Sequence: 1 MRPSTQFLGLLFWLHGACQ YCLQYDNLWTFGGGTLEIK 126

Scoring table: BLCSUM62
Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
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2	539	79.3	361	12	US-10-335-394-13	Sequence 13, Appl
3	535	78.7	374	12	US-10-335-394-15	Sequence 15, Appl
4	490	72.1	109	9	US-09-229-200A-17	Sequence 7, Appl
5	482.5	71.0	108	9	US-09-229-200A-17	Sequence 17, Appl
6	481.5	70.8	131	15	US-10-207-655-256	Sequence 256, Appl
7	481.5	70.8	266	15	US-10-207-655-60	Sequence 260, Appl
8	481.5	70.8	550	15	US-10-207-655-70	Sequence 270, Appl
9	445.5	65.5	127	12	US-10-268-883-5	Sequence 5, Appl
10	442.5	65.1	236	15	US-09-859-53-0	Sequence 30, Appl
11	441	64.9	241	15	US-10-221-945-1	Sequence 1, Appl
12	437.5	64.3	131	8	US-08-779-784-21	Sequence 21, Appl
13	434.5	64.0	234	9	US-09-740-002-24	Sequence 24, Appl
14	434.5	63.9	128	9	US-09-764-304-10	Sequence 10, Appl
15	434.5	63.9	128	9	US-09-764-304-19	Sequence 19, Appl

SEQUENCES

16	434.5	63.9	128	12	US-10-166-626-10	Sequence 10, Appl
17	434.5	63.9	128	12	US-10-166-626-19	Sequence 10, Appl
18	434.5	63.9	128	15	US-10-265-713-10	Sequence 19, Appl
19	434.5	63.9	128	15	US-10-265-713-19	Sequence 11, Appl
20	431.5	63.5	108	9	US-09-229-200A-11	Sequence 15, Appl
21	431.5	63.5	108	9	US-09-229-200A-15	Sequence 16, Appl
22	429.5	63.5	108	9	US-09-229-200A-16	Sequence 71, Appl
23	429.5	63.2	127	15	US-10-084-139-71	Sequence 2, Appl
24	424.5	62.4	127	15	US-10-084-139-71	Sequence 4, Appl
25	424.5	62.4	259	12	US-10-053-530-13	Sequence 13, Appl
26	424.5	62.4	259	15	US-10-207-655-13	Sequence 150, App
27	420.5	61.8	234	9	US-09-800-729-150	Sequence 2, Appl
28	418.5	61.5	142	9	US-09-844-736-4	Sequence 4, Appl
29	418.5	61.5	142	15	US-10-162-336-4	Sequence 7, Appl
30	418.5	61.5	142	15	US-10-162-336-4	Sequence 100, App
31	417.5	61.4	127	15	US-10-283-349-88	Sequence 2, Appl
32	416.5	61.3	127	14	US-10-011-125-2	Sequence 88, Appl
33	416	61.2	234	9	US-09-740-002-26	Sequence 26, Appl
34	414.5	61.0	128	9	US-09-855-771-26	Sequence 1, Appl
35	413.5	60.8	125	10	US-09-809-739-1	Sequence 6, Appl
36	413.5	60.8	127	15	US-10-084-139-6	Sequence 100, App
37	413	60.7	237	9	US-09-056-160B-100	Sequence 2, Appl
38	413	60.7	491	14	US-10-125-2	Sequence 8, Appl
39	412.5	60.7	127	12	US-10-289-181-8	Sequence 73, Appl
40	411.5	60.5	108	9	US-09-905-243-73	Sequence 26, Appl
41	410.5	60.4	107	12	US-10-330-613-16	Sequence 26, Appl
42	410.5	60.4	107	12	US-10-330-530-26	Sequence 17, Appl
43	410.5	60.4	127	15	US-10-283-349-92	Sequence 17, Appl
44	409.5	60.2	127	15	US-10-283-349-92	Sequence 92, Appl
45	407.5	59.9	107	9	US-09-056-160B-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1	US-10-335-394-16	US-10-335-394-16	US-10-335-394-16	US-10-335-394-16	US-10-335-394-16	US-10-335-394-16
;	SEQUENCE 16, Application US/10335394	;	SEQUENCE 16, Application US/10335394	;	SEQUENCE 16, Application US/10335394	;
;	GENERAL INFORMATION:	;	GENERAL INFORMATION:	;	GENERAL INFORMATION:	;
;	APPLICANT: Kwak, Larry	;	APPLICANT: Birazyan, Artya	;	APPLICANT: Birazyan, Artya	;
;	;	;	TITLE OF INVENTION: METHODS AND COMPOSITIONS OF	;	TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES	;
;	;	;	FILE REFERENCE: 14014_0316.P	;	CURRENT APPLICATION NUMBER: US/10/335,394	;
;	;	;	CURRENT FILING DATE: 2002-12-31	;	PRIOR APPLICATION NUMBER: US/09/646,028	;
;	;	;	PRIOR FILING DATE: 2000-09-12	;	PRIOR FILING DATE: 2000-09-12	;
;	;	;	PRIOR APPLICATION NUMBER: 60/077,745	;	PRIOR APPLICATION NUMBER: 60/077,745	;
;	;	;	NUMBER OF SEQ ID NOS: 57	;	NUMBER OF SEQ ID NOS: 57	;
;	;	;	SEQ ID NO: 16	;	SEQ ID NO: 16	;
;	;	;	LENGTH: 359	;	LENGTH: 359	;
;	;	;	TYPE: PRT	;	TYPE: PRT	;
;	;	;	ORGANISM: Artificial sequence	;	ORGANISM: Artificial sequence	;
;	;	;	FEATURE:	;	FEATURE:	;
;	;	;	OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct	;	OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct	;

QY	17	GAQDIONTOSPSLSSASLGKKTICKTSODINKYAMYQHKPGKPRPLIHYTSALOP 76
Db	229	GSSDIONTQSSSLSSASLGKKTICKTSODINKYAMYQHKPGKPRPLIHYTSALOP 288
QY	77	GIPSREFSGSGSGRDYSFNISNLPEPDIATYCLQDNLWTFGGTKLEIK 126
Db	289	GIPSREFSGSGSGRDYSFNISNLPEPDIATYCLQDNLWTFGGTKLEIK 338

RESULT 2
US-10-335-394-13
Sequence 13, Application US/10335394
Publication No. US20030138452A1
GENERAL INFORMATION:
APPLICANT: Kwak, Larry
ORGANISM: Biragyn, Arya
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
FILE REFERENCE: 14014.0316/P
CURRENT APPLICATION NUMBER: US/10/335,394
CURRENT FILING DATE: 2002-12-31
PRIOR APPLICATION NUMBER: US/09/646,028
PRIOR FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745
PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 13
LENGTH: 361
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-10-335-394-13

Query Match 79.3%; Score 539; DB 12; Length 361;
Best Local Similarity 91.8%; Pred. No. 6.2e-42;
Matches 101; Conservative 4; Mismatches 5; Indels 0;
Query 17 GAQCDIQMTQSPSSLASLGGKVTTICKTSQDINKYMAWQHKPGKPRLLHYTSLQP 76
Db 231 GSGCDIQMTQSPSSLASLGGKVTTICKTSQDINKYIAWQHKPGKPRLLHYTSLQP 290
Query 77 GIPSRFGSGSGRDYSFNTSNEPEDATYCLQYDNILWTFGGTLEIK 126
Db 291 GIPSRFGSGSGRDYSFNTSNEPEDATYCLQYDNLYTFGGTLEIK 340

RESULT 3
US-10-335-394-15
Sequence 15, Application US/10335394
Publication No. US20030138452A1
GENERAL INFORMATION:
APPLICANT: Kwak, Larry
ORGANISM: Biragyn, Arya
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
FILE REFERENCE: 14014.0316/P
CURRENT APPLICATION NUMBER: US/10/335,394
CURRENT FILING DATE: 2002-12-31
PRIOR APPLICATION NUMBER: US/09/646,028
PRIOR FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745
PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 15
LENGTH: 374
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-10-335-394-15

Query Match 78.7%; Score 535; DB 12; Length 374;
Best Local Similarity 94.3%; Pred. No. 1.5e-41;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Caps 0;
Query 21 DIQMTQSPSSLASLGGKVTTICKTSQDINKYIAWQHKPGKPRLLHYTSLQP 80
Db 95 DIQMTQSPSSLASLGGKVTTICKTSQDINKYIAWQHKPGKPRLLHYTSLQP 154

RESULT 4
US-09-229-200A-7
Sequence 7, Application US/09229200A
Patent No. US20030099179A1
GENERAL INFORMATION:
APPLICANT: Jolliffe et al.
TITLE OF INVENTION: CD4 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Johnson & Johnson
STREET: One Brunswick & Johnson Plaza
CITY: New Brunswick
STATE: NJ
COUNTRY: USA
ZIP: 08933-7003
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/229,200A
FILING DATE: 13-Jan-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: John W. Wallen, III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: ORT-948
TELECOMMUNICATION INFORMATION:
TELEPHONE: (856)1784-3239
TELEFAX: (908)524-2808
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 109
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-229-200A-7

Query Match 72.1%; Score 490; DB 9; Length 109;
Best Local Similarity 86.1%; Pred. No. 5.6e-38;
Matches 93; Conservative 8; Mismatches 5; Indels 2; Gaps 1;
Query 21 DIQMTQSPSSLASLGGKVTTICKTSQDINKYMAWQHKPGKPRLLHYTSLQP 80
Db 1 DIQMTQSPSSLASLGGKVTTACKASQDINKYIAWQHKPGKPRLLHYTSLQP 60
Query 81 RFSGSGSGRDYSFNTSNEPEDATYCLQYDNILWTFGGTLEIK 126
Db 61 RFSGSGSGRDYSFNTSNEPEDATYCLQYDNLYTFGGTLEIK 108
RESULT 5
US-09-229-200A-17
Sequence 17, Application US/09229200A
Patent No. US20030099179A1
GENERAL INFORMATION:
APPLICANT: Jolliffe et al.
TITLE OF INVENTION: CD4 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Johnson & Johnson
STREET: One Johnson & Johnson Plaza
CITY: New Brunswick
STATE: NJ
COUNTRY: USA
ZIP: 08933-7003

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 78.7%; Score 535; DB 2; Length 104;
Best Local Similarity 95.2%; Pred. No. 2.3e-39;
Matches 99; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 21 DIQMTQSPSSLSAISGGKVTTCKTSQDINKYMAWWQHKPGRPRLLIHTSALQGIPS 80
Db 1 DIQMTQSPSSLSAISGGKVTTCKTSQDINKYMAWWQHKPGRPRLLIHTSALQGIPS 60

Qy 81 RFSGSGSGRDYSFNISNLEPDIATYCLQDNLWTFGGTKE 124
Db 61 RFSGSGSGRDYSFNISNLEPDIATYCLQDNLWTFGGTKE 104

RESULT 3

S26329 Ig kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26329
R;Shark, S.E.; Catton, A.J.
J;Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e
A;Reference number: S26309; MUID:9134121; PMID:1908510
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-104 <STA>
A;Cross-references: EMBL:X59173; NID:952309; PIDN:CAA41883.1; PID:91334059
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 77.4%; Score 526; DB 2; Length 104;
Best Local Similarity 94.2%; Pred. No. 1.3e-38;
Matches 98; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 21 DIQMTQSPSSLSAISGGKVTTCKTSQDINKYMAWWQHKPGRPRLLIHTSALQGIPS 80
Db 1 DIQMTQSPSSLSAISGGKVTTCKTSQDINKYMAWWQHKPGRPRLLIHTSALQGIPS 60

Qy 81 RFSGSGSGRDYSFNISNLEPDIATYCLQDNLWTFGGTKE 124
Db 61 RFSGSGSGRDYSFNISNLEPDIATYCLQDNLWTFGGTKE 104

RESULT 4

C33936 Ig kappa chain V region (VM13) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 01-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C;Accession: C33936
R;Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989
A;Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene
A;Reference number: A33936; MUID:89282831; PMID:2471975
A;Accession: C33936
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-106 <ME>
A;Cross-references: GB:J04577; NID:9623187; PIDN:RAA60443.1; PID:9623189
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 77.1%; Score 524; DB 2; Length 106;
Best Local Similarity 91.5%; Pred. No. 2e-38;
Matches 97; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 21 DIQMTQSPSSLSAISGGKVTTCKTSQDINKYMAWWQHKPGRPRLLIHTSALQGIPS 80
Db 1 DIQMTQSPSSLSAISGGKVTTCKTSQDINKYMAWWQHKPGRPRLLIHTSALQGIPS 60

Qy 81 RFSGSGSGRDYSFNISNLEPDIATYCLQDNLWTFGGTKE 126
Db 61 RFSGSGSGRDYSFNISNLEPDIATYCLQDNLWTFGGTKE 106

RESULT 5

S52789 Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52789
R;Rocca, A.; Khamiuchi, A.A.; Touchard, G.; Mogenot, B.; Ronco, P.; Denoy, L.; Del submitted to the EMBL Data Library, March 1995
A;Description: Light chain V region gene usage restriction and peculiarities in myelc
A;Reference number: S52789
A;Accession: S52789
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-129 <ROC>
A;Cross-references: EMBL:X85995; NID:9758588; PIDN:CAA59987.1; PID:9758589
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 72.1%; Score 490.5; DB 2; Length 129;
Best Local Similarity 72.4%; Pred. No. 1.9e-35;
Matches 92; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

Qy 1 MRPSTQFLGLLFLWHLGAQDIDOMTQSPSSLSAISGGKVTTCKTSQDINKYMAWWQHKP 60
Db 3 MRPQAQLGLLFLWHLSGARDQMTQSPSSLSAISGGKVTTCKTSQDINKYMAWWQHKP 62

Qy 61 GKRPLIHTSALQPGTSPSRSGSGRDSYDSEFIDATYCLQDNLWTFGG 119
Db 63 GAKPLLTAASSLETGVSPRSFGSGSCTDFSETTISLQPEDLATYCOOYDNPLTFGG 122

Qy 120 GTKLEIK 126
Db 123 GTKYEIK 129

RESULT 6

S26332 Ig light chain V region - mouse (fragment)
N;Alternate names: Ig kappa chain V region
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
C;Accession: S26332; S26331
R;Stark, S.E.; Caton, A.J.
J;Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26332
A;Molecule type: mRNA
A;Residues: 1-103 <STA>
A;Cross-references: EMBL:X59191; NID:952321; PIDN:CAA41901.1; PID:91334066
C;Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 72.1%; Score 490; DB 2; Length 103;
Best Local Similarity 87.4%; Pred. No. 1.7e-35;
Matches 90; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 21 DIQMTQSPSSLSAISGGKVTTCKTSQDINKYMAWWQHKPGRPRLLIHTSALQGIPS 80
Db 1 DIQMTQSPSSLSAISGGKVTTCKTSQDINKYMAWWQHKPGRPRLLIHTSALQGIPS 60

Result No.	Query	Score	Match	Length	DB	ID	Description
1	441.5	64.9	129	1	KV1B_HUMAN	P04431	homo sapien
2	425.5	62.6	128	1	KV5E_MOUSE	P01637	mus musculu
3	412.5	60.7	129	1	KV1X_HUMAN	P04432	homo sapien
4	402	59.1	117	1	KV1J_HUMAN	P01630	homo sapien
5	400	58.8	115	1	KV5F_MOUSE	P01638	mus musculu
6	397.5	58.5	108	1	KV1B_HUMAN	P01594	homo sapien
7	395.5	58.2	108	1	KV1G_HUMAN	P01607	homo sapien
8	392.5	57.7	108	1	KV1P_HUMAN	P01608	homo sapien
9	389.5	57.3	108	1	KV1Y_HUMAN	P080362	homo sapien
10	380.5	56.0	108	1	KV1A_HUMAN	P01593	homo sapien
11	379.5	55.8	108	1	KV1M_HUMAN	P01605	homo sapien
12	378.5	55.7	130	1	KV5G_MOUSE	P01639	mus musculu
13	378.5	55.7	133	1	KV4B_HUMAN	P06313	homo sapien
14	378	55.6	117	1	KV1I_HUMAN	P01601	homo sapien
15	377.5	55.5	108	1	KV5J_MOUSE	P01643	mus musculu
16	377	55.4	107	1	KV1D_HUMAN	P01596	homo sapien
17	375	55.1	134	1	KV4C_HUMAN	P06314	homo sapien
18	374.5	55.1	108	1	KV5O_MOUSE	P01648	mus musculu
19	373.5	54.9	108	1	KV1Q_HUMAN	P01609	homo sapien
20	373.5	54.9	108	1	KV5N_MOUSE	P01647	mus musculu
21	371.5	54.6	108	1	KV5K_MOUSE	P01644	mus musculu
22	369.5	54.3	108	1	KV5M_MOUSE	P01646	mus musculu
23	368.5	54.2	108	1	KV5L_MOUSE	P01645	mus musculu
24	366.5	53.9	108	1	KV1R_HUMAN	P01610	homo sapien
25	362.5	53.3	108	1	KV1C_HUMAN	P01595	homo sapien
26	360.5	53.0	108	1	KV1H_HUMAN	P01600	homo sapien
27	359.5	52.9	108	1	KV1N_HUMAN	P01606	homo sapien
28	357.5	52.6	108	1	KV1E_HUMAN	P01597	homo sapien
29	357.5	52.6	108	1	KV1V_HUMAN	P04430	homo sapien
30	355.5	52.3	108	1	KV1F_HUMAN	P01598	homo sapien
31	353.5	52.1	108	1	KV1S_HUMAN	P01611	homo sapien
32	353.5	52.0	115	1	KV5C_MOUSE	P01635	mus musculu
33	352.5	51.8	108	1	KV1K_HUMAN	P01603	homo sapien

ALIGNMENTS						
RESULT 1						
KV1W_HUMAN						
ID	KV1W_HUMAN		STANDARD;		PRT;	129 AA.
AC	P04431;					
DT	13-AUG-1987 (Rel. 05, Created)					
DT	13-AUG-1987 (Rel. 05, Last annotation update)					
DT	15-JUL-1999 (Rel. 38, Last annotation update)					
DE	Ig kappa chain V-I region Walker precursor.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX	NCBI_TaxID-9606;					
RN	11]					
RP	SEQUENCE FROM N.A.					
RX	MEIDLINE-85014148; PubMed-6091049;					
RA	Klobeck H.G.; Combrato G.; Zachau H.G.;					
RT	"Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines are closely related."					
RL	Nucleic Acids Res. 12:6995-7006(1984).					
CC	CC					
CC	CC					
CC	CC					
CC	CC					
CC	CC					
CC	CC					
CC	CC					
DR	X00965: CAA25477-1; ALT TERM.					
DR	DRTR; A01682; KIHWK.					
DR	HSPP; P01667; IREB.					
DR	GO; GO:0005276; C: extracellular.					
DR	GO; GO:0005823; F: antigen binding activity.					
DR	GO; GO:0009823; F: immunoglobulin binding activity.					
DR	GO; GO:000955; P: immune response.					
DR	DR; InterPro; IPR007110; Ig-like.					
DR	InterPro; IPR003006; Ig_MHC.					
DR	InterPro; IPR003596; Ig_V.					
DR	PFAM; PF00474; Ig_V.					
DR	SMART; SM00406; IgV.					
DR	PROSITE; PS050835; Ig_LIKE.					
KW	Immunoglobulin V region; signal.					
FT	Immunoglobulin V region; signal.	1	22			
FT	CHAIN	23	129	IG KAPPA CHAIN V-I REGION WALKER.		
FT	DOMAIN	23	45	FRAMWORK-1.		
FT	DOMAIN	46	56	COMPLEMENTARITY-DETERMINING-1.		
FT	DOMAIN	57	71	FRAMWORK-2.		
FT	DOMAIN	72	78	COMPLEMENTARITY-DETERMINING-2.		
FT	DOMAIN	79	110	FRAMWORK-3.		
FT	DOMAIN	111	119	COMPLEMENTARITY-DETERMINING-3.		
FT	DOMAIN	120	129	FRAMWORK-4.		
FT	DISULFID	45	110	BY SIMILARITY.		
FT	NON_TER	129	129			
SQ	SEQUENCE	129 AA;	14 0469 MW;	F941FA07D4AFC2F9 CRC64;		
Query Match				Score 441.5; DB 1; Length 129;		
Best Local Similarity				Pred. No. 1.7e-38;		

Matches 85; Conservative 15; Mismatches 26; Indels 1; Gaps 1; QY 1 MRPSQFLGILMLHGAQCDIOMTQPSLSSAISLOGKVITCKTSODINKYMAWYQK 60
3 MRVPAQLGULLWLGRARCQDIOMTQPSLSSAISVGRTVITCRASOSISNYQQK 62

QY 61 GKRPRLLIHTYTSALQPGIPSREFSGSGRDSYNSNLEPDIATYCLQ-YDNWTFGG 119
63 GKAFLILLYAASSLQSCVYTSRPSGSGSSTDFLTISLQPESSATYQCSYSTLTFGG 122

QY 120 GTKLEIK 126
121 GTKLEIK 129
Db 123 GTKLEIK 129

RESULT 2 KV5E MOUSE STANDARD; PRT; 128 AA.
ID KV5E_MOUSE STANDARD; PRT; 128 AA.
AC P01637; 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-V region T1 precursor.
OS Mus musculus (Mouse).
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.
OX NCBI_TAXID=10090;
RN SEQUENCE FROM N.A.
RP MEDLINE-#1053342; PubMed-6776411;
RX RT "Functional and non-functional joining in immunoglobulin light chain genes of a mouse myeloma.";
RT RT Nature 287:603-607(1980).
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CC EMBL; V00772; CAA24150.1; -.
CC DR PIR; A01920; KVMST1.
DR HSSP; PB0362; IWTL.
DR InterPro; IPR07110; Ig-like.
DR InterPro; IPR03006; Ig_MHC.
DR InterPro; IPR03596; Ig_V.
Pfam; PF00047; ig; 1.
DR SMART; SM00405; Ig; 1.
DR PROSITE; PS50335; Ig_LIKE; 1.
DR PROSITE; PS50335; Ig_LIKE; 1.
DR NON_TER; 14395 MW; AF0563D31BB7E05 CRC64;
SQ SEQUENCE 128 AA; 14395 MW; AF0563D31BB7E05 CRC64;

Query Match 62 6%; Score 425.5; DB 1; Length 128;
Best Local Similarity 62 2%; Pred. No. 7.5e-37;
Matches 79; Conservative 18; Mismatches 29; Indels 1; Gaps 1;

QY 1 MRPSQFLGILMLHGAQCDIOMTQPSLSSAISLOGKVITCKTSODINKYMAWYQK 60
1 MRTPAQLGULLWLGRARCQDIOMTQPSLSSAISVGRTVITCRASOSISNYQQK 62

Db 61 GKRPRLLIHTYTSALQPGIPSREFSGSGRDSYNSNLEPDIATYCLQ-YDNWTFGG 119
61 GKRPRLLIHTYTSALQPGIPSREFSGSGRDSYNSNLEPDIATYCLQ-YDNWTFGG 120
QY 120 GTKLEIK 126
Db 121 GTKLEIK 127

RESULT 3 KV5X_HUMAN STANDARD; PRT; 129 AA.
ID KV5X_HUMAN STANDARD; PRT; 129 AA.
AC P04432; 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Daudz precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TAXID=9506;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-#501148; PubMed-6091049;
RA Klobbeck H.G.; Combrutto G.; Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines are closely related.;"
RT Nucleic Acids Res. 12:6995-7005(1984).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC DR X00966; CAA25478.1; ALT_TERMM.
DR PIR; A01884; KIHUDI.
DR HSSP; PB0362; IWTL.
DR GO; GO:000576; C_extracellular; NAS.
DR GO; GO:0003823; F_antigen binding activity; NAS.
DR GO; GO:0006955; P_immunogen response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR03006; Ig_MHC.
DR InterPro; IPR03596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00405; Ig; 1.
DR PROSITE; PS50835; Ig_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 23 129
FT DOMAIN 23 45
FT FRAMEWORK-1. 46 56
FT DOMAIN-1. 57 71
FT DOMAIN 72 78
FT DOMAIN 79 110
FT DOMAIN 111 119
FT DOMAIN 120 129
FT DISULFID 45 119
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14335 MW; CAF076BC7E5574C8 CRC64;

Query Match 60 7%; Score 412.5; DB 1; Length 129;
Best Local Similarity 61 4%; Pred. No. 1.e-35;
Matches 78; Conservative 19; Mismatches 29; Indels 1; Gaps 1;

QY 1 MRPSQFLGILMLHGAQCDIOMTQPSLSSAISLOGKVITCKTSODINKYMAWYQK 60
3 MRVPAQLGULLWLGRARCQDIOMTQPSLSSAISVGRTVITCRASOSISNYQQK 62

Db 61 GKRPRLLIHTYTSALQPGIPSREFSGSGRDSYNSNLEPDIATYCLQ-YDNWTFGG 119
QY

GenCore version 5.1.6
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protein - protein search, using sw model

on: October 7, 2003, 09:01:50 ; search time 61.0909 Seconds
 (without alignments)
 363.748 Million cell updates/sec

US-09-155-739-4

refact score: 746

sequence: 1 MKCSWVMAFFLMAVVTGYNSE YGNYYGAMYDWGQGTSTVTY 140

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title: US-09-155-739-4
refct score: 746
sequence: 1 MRCSWVWFFLMAVVTCYNSE . . . . . YGNQGYVAMDYWGQGTSTVY 140
oring table: BL0SUM62
Gapop 10.0 , Gapext 0.5
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total number of hits satisfying chosen parameters: 1107863
minimum DB seq length: 0
maximum DB seq length: 200000000
post-processing: Minimum Match 0%
Maximum Match 100%
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2: /SIDS1/gcdata/geneset/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS1/gcdata/geneset/geneseq/geneseqp-emb1/AA1982.DAT:*
4: /SIDS1/gcdata/geneset/geneseq/geneseqp-emb1/AA1983.DAT:*
5: /SIDS1/gcdata/geneset/geneseq/geneseqp-emb1/AA1984.DAT:*

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SUMMARIES				
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2	746	100.0	140	AAR22410
3	645	96.5	123	AAR81330
4	633	84.9	136	AAR04379
5	629	84.3	140	AAR11384
6	625	83.8	136	AAR76664
7	595	79.8	136	AAR41679
8	593	79.6	137	AAR21845
9	591	79.2	138	AAR63828

10	584	78.3	142	16	AAR81333
11	584	78.3	142	18	AAW22428
12	576.5	77.3	135	21	AAB07967
13	570.5	76.5	137	17	AAR81548
14	544	72.9	123	16	AAR81323
15	539.5	72.3	125	15	AAB07967
16	537	72.0	123	18	AAW22413
17	535.5	71.8	437	21	AAW37738
18	527	70.6	119	24	ABP97550
19	524.5	70.3	122	21	AAY53590
20	521.5	69.9	120	19	AAR30767
21	521.5	69.9	120	19	AAW44121
22	521.5	69.9	120	23	AAU79031
23	518.5	69.5	113	15	AAR60527
24	517	69.3	143	15	AAR5942
25	516.5	69.2	120	16	AAR79889
26	516.5	69.2	150	24	AAE33371
27	516	69.2	121	20	AAW96744
28	516	69.2	121	24	ABU08538
29	513	68.6	121	24	AAW96744
30	513	68.8	121	24	ABU08543
31	513	68.8	138	22	AAG66455
32	511	68.5	120	14	AAR39817
33	511	68.5	120	15	AAR58749
34	511	68.5	120	20	AAZ23984
35	511	68.5	120	20	AAY01033
36	511	68.5	120	22	ABT73462
37	509.5	68.3	126	12	AAR15439
38	508	68.1	120	14	AAR39666
39	507.5	68.0	133	23	ABB75617
40	505.5	67.8	138	18	AAW56873
41	505.5	67.8	139	18	AAW29753
42	504	67.6	254	20	AAY30117
43	504	67.6	254	20	AAZ30117
44	504	67.6	254	20	AAY30121

ALIGMENTS

able region. scule; VLA-4; therapeutic;

Human VLA-4	reshap
Humanised alpha-4	
Amino acid sequenc	
HNK-20 variable he	
Humanized VLA-4 an	
A heavy chain vari	
Humanised alpha-4	
Nucleotide sequenc	
Amino acid sequenc	
Heavy chain from a	
Heavy chain variab	
Anti-VLA44	rb huma
Anti-EGFR	anti-ibody
Ryridoma 902	immu
Heavy chain variab	
Mouse anti-VLA-4	a
Heavy chain variab	
Mouse anti-VLA-4	a
VEGF ScFv protein	
HP1/2	vn
Anti-VLA4	Ab HP1/2
Antibody	HP1/2
Anti VLA-4	antibod
Murine anti-VLA-4	
Heavy chain variab	
Sequence of the va	
Anti-RANK ligand m	
MAB CT-M-01	heavy
Anti-HMFG MAB CTM0	
Murine anti-botul	
Murine anti-botul	
Murine anti-botul	

W09519790-A1.	XX	transplant rejection; graft versus host disease; nephritis; atopic dermatitis; psoriasis; myocardial ischaemia; acute leukocyte mediated lung injury; therapy.
27-JUL-1995.	XX	
25-JAN-1995; 95WO-US01219.	XX	
25-JAN-1994; 94US-0186269.	XX	
(ATHÈ-) ATHENA NEUROSCIENCES INC.	XX	
Bendig MM, Jones TS, Leger OJ, Saldanha J;	XX	
WPI; 1995-262276/35.	XX	
N-PSDB; AAQ99892.	XX	
New humanised antibodies against VLA-4 - used for inhibiting leukocyte adhesion to endothelial cells, partic. for treating inflammatory disease.	XX	
Disclosure: Fig 2: 105pp; English.	XX	
The sequence represents the mouse antibody 21.6 heavy chain variable region directed against leukocyte adhesion molecule VLA-4. Cloned cDNA sequences of mouse 21.6 VH and VL (see AAQ998891) regions are linked to human constant regions in the construction of a humanized antibody against VLA-4. The 5', and 3' ends of the mouse cDNAs are modified using PCR primers (See AAQ99895-98) and then subcloned into mammalian cell expression vectors containing human kappa or gamma-1 constant regions. In the humanized heavy chain, amino acids H27, H28, H29, H30, H4 and H71 in the human HC VR framework are replaced by the amino acid present in the equivalent position of the mouse 21.6 Ig H chain. Plasmids encoding the chimeric antibodies are transfected into COS cells. The humanized antibodies can be used to inhibit adhesion of a leukocyte to an endothelial cell, and to treat inflammatory diseases such as multiple sclerosis, They can also be used in the treatment of stroke, cerebral traumas, meningitis or encephalitis. The antibodies can also be used for detecting VLA-4, for affinity purification or for generating anti-idiotypic antibodies.	XX	
Sequence 140 AA;	XX	
Query Match 100.0%; Score 746; DB 16; Length 140;	XX	
Best Local Similarity 100.0%; Pred. No. 1e-59;	XX	
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	
QY 1 MKCSRMVMEFLMAYVGVNEVQLOQSGAELVKPGASVKSCTASGFNIMDTYIHCVKRGP 60	Db	
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61 EQGLEWIGRIDPANGTYKDPKFQGKATTAIDTSNTAYTQLQSSLTSETAVFCARESY 120	QY	
61 EQGLEWIGRIDPANGTYKDPKFQGKATTAIDTSNTAYTQLQSSLTSETAVFCARESY 120	Db	
QY 121 YGNGYTYADYWGQTSVY 140	Db	
121 YGNGYTYADYWGQTSVY 140	Db	
08-DEC-1997 (first entry)	XX	
RESULT 2	XX	
AAW22410	DE	
XX	DE	
Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; diabetes; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis;	XX	
Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; asthma; atherosclerosis; AIDS; dementia; tumour; metastasis; inflammatory bowel disease; rheumatoid arthritis;	XX	
Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6; best local similarity 100.0%; pred. No. 1e-59;	XX	
Matches 140; conservative 0; mismatches 0; indels 0; sequence 140 AA;	XX	
Query Match 100.0%; Score 746; DB 18; length 140;	XX	

Result No.	Score	Query Match	Length	DB ID	Description
1	746	100.0	140	2	US-08-561-521-4
2	746	100.0	140	5	PCT-US93-00924-2
3	645	86.5	123	2	US-08-561-521-9
4	645	86.5	123	5	PCT-US93-01219-9
5	633	84.9	136	3	US-08-664-265A-29
6	595	79.8	136	1	US-08-024-253-2
7	593.5	79.6	137	3	US-08-836-561-31
8	593.5	79.6	137	4	US-05-034-122-31
9	584	78.3	142	2	US-08-561-521-17
10	584	78.3	142	5	PCT-US93-01219-17
11	562	75.3	125	2	US-08-561-521-44
12	562	75.3	125	5	PCT-US93-01219-44
13	554	74.3	136	3	US-08-838-561-8
14	554	74.3	136	5	PCT-US93-15716-8
15	544	72.9	123	2	US-08-561-521-11
16	544	72.9	123	5	PCT-US93-01219-11
17	528.5	70.8	120	2	US-07-934-37C-6
18	528.5	70.8	120	3	US-08-437-642B-6
19	528.5	70.8	120	4	US-08-146-20C-6
20	528.5	70.8	120	5	PCT-US93-07832-6
21	521.5	69.9	120	4	US-08-871-488A-15
22	516	69.2	121	2	US-08-822-830B-2
23	516	69.2	121	4	US-09-157-452B-2
24	513	68.8	121	2	US-08-822-830B-13
25	513	68.8	121	4	US-09-157-452B-16
26	511	68.5	120	2	US-08-930-660-2
27	511	68.5	120	5	PCT-US93-00030-2

Qy 1 MKCSWMMFFLMAVTVGYNSEVQLOQSGAELVKPGASVKLSCASGNIKDTYIHCVKQRP 60
 Db 1 MKCSWMMFFLMAVTVGYNSEVQLOQSGAELVKPGASVKLSCASGNIKDTYIHCVKQRP 60

RESULT 3
 US-08-561-521-9

Sequence 9, Application US/08561521
 Patent No. 5840299

GENERAL INFORMATION:

APPLICANT: Bendig, Mary M.
 APPLICANT: Leger, Olivier J.
 APPLICANT: Salданha, Jose
 APPLICANT: Jones, S. Tarran

TITLE OF INVENTION: Humanized Antibodies Against Leukocyte

TITLE OF INVENTION: Adhesion Molecule VLA-4

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew
 STREET: One Market Plaza, Steuart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/01219
 FILING DATE: 25-JAN-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/186,269A
 FILING DATE: 25-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William L.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 15270-14

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-543-9600
 TELEFAX: 415-543-5443

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 123 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-561-521-9

Query Match 86.5%; Score 645; DB 2; Length 123;
 Best Local Similarity 100.0%; Pred. No. 3-5e-58;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 EYQIQQSGAELVPGASVKLSCASGNIKDTYIHCVKQRP 79
 Db 1 EYQIQQSGAELVPGASVKLSCASGNIKDTYIHCVKQRP 79

Qy 80 DPKEQGKATITATSSNTAYLQLSSISEDTAVYFCAREGYGNYCANDYWGQTSVT 139
 Db 61 DPKEQGKATITATSSNTAYLQLSSISEDTAVYFCAREGYGNYCANDYWGQTSVT 120

RESULT 4
 PCT/US95-01219-9

Sequence 9, Application PC/TUS9501219
 GENERAL INFORMATION:

APPLICANT: Bendig, Mary M.
 APPLICANT: Leger, Olivier J.
 APPLICANT: Salданha, Jose

Qy 121 YGNYGYAMDYWGQTSVT 140
 Db 121 YGNYGYAMDYWGQTSVT 140

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OM protein - protein search, using sw model

Run on: October 7, 2003, 09:18:36 ; Search time 35.355 Seconds
(without alignments)
626.523 Million cell updates/sec

Title: US-09-155-739-4
Perfect score: 746

Sequence: 1 MKCSWVMMFFLMVVTGVNRE.YNYGYAMDWQGQNSVTY 140

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters : 587654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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18: /cgns2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	633	89.9	136	11	US-09-749-873-29	Sequence 29, Appl
2	593.5	79.6	137	15	US-10-319-31	Sequence 31, Appl
3	521.5	69.9	120	15	US-10-056-794-15	Sequence 15, Appl
4	516	69.2	121	15	US-10-252-978-2	Sequence 2, Appl
5	513	68.8	121	15	US-10-232-978-16	Sequence 16, Appl
6	511	68.5	120	15	US-10-095-456-1	Sequence 1, Appl
7	502	67.3	136	11	US-09-749-873-99	Sequence 99, Appl
8	495.5	66.4	116	11	US-19-910-483-37	Sequence 37, Appl
9	495.5	66.4	116	11	US-09-910-483-41	Sequence 41, Appl
10	491.5	65.9	255	10	US-09-910-059-19	Sequence 19, Appl
11	488.5	65.5	136	9	US-09-564-3294-1	Sequence 11, Appl
12	488.5	65.5	136	10	US-09-855-154-11	Sequence 11, Appl
13	488.5	65.5	136	10	US-09-854-811-11	Sequence 11, Appl
14	488.5	65.5	136	10	US-09-914-773-11	Sequence 11, Appl
15	488.5	65.5	136	10	US-09-963-620-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-749-873-29

; Sequence 29, Application US/09749873

; Publication No. US20030023045A1

; GENERAL INFORMATION:

APPLICANT: OHOMO, Toshihiko

SATO, Koh

TSUCHIYA, Masayuki

TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN

MEDULLOBLASTOMA CELLS

NUMBER OF SEQUENCES: 132

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/749, 873

FILING DATE: 19-NOV-1993

FILING DATE: 29-Dec-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/646,265

FILING DATE: 1996-09-09

APPLICATION NUMBER: JP 5-291078

FILING DATE: 19-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: WEGNER, Harold C.

REGISTRATION NUMBER: 25,258

REFERENCE/DOCKET NUMBER: 53466/184

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202)672-5399
 TELE: 904.136
 INFORMATION FOR SEQ ID NO: 29:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 136 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 29:
 US-09-749-873-29

Query Match	84.9%	Score 633;	DB 11;	Length 136;
Best Local Similarity	89.3%	Pred. No. 3.1e-56;	Indels 6;	Gaps 2;
Matches	125;	Conservative	2;	Mismatches 7;

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 Db 1 MKCSWVMAFFLMAVVGVNSEVQLOQSGAELVKPGASVKSCTASSENFNIKDTYHCKQRP 60

QY 61 EQGLEWIGRIDPANGTYKDPKFQGRATITADTSNTAYQLQSSLTSEDTAVYFCAREGY 120
 Db 61 EQGLEWIGRIDPANGTYKDPKFQGRATITADTSNTAYQLQSSLTSEDTAVYFCAREGY 120

QY 61 EQGLEWIGRIDPANGTYKDPKFQGRATITADTSNTAYQLQSSLTSEDTAVYFCAREGY 120
 Db 61 EQGLEWIGRIDPANGTYKDPKFQGRATITADTSNTAYQLQSSLTSEDTAVYFCAREGY 120

QY 121 YGNYGYAMDWQGQTSVY 140
 Db 121 YGNYGYAMDWQGQTSVY 140

QY 120 YVN----QDYGQGQTSVY 134
 Db 120 YVN----QDYGQGQTSVY 134

RESULT 3
 US-10-056-794-15

RESULT 2
 US-10-283-349-31

Sequence 31, Application US/10283349
 Publication No. US20030096977A1

GENERAL INFORMATION:
 APPLICANT: KOIKE, Masamichi
 FURUTA, Atsuko
 NAKANDRA, Kazuyasu
 TIDA, Akiniro
 ANAZAWA, Hideharu
 HANAI, No. US20030096977A1
 TAKAYOSU, Kiyoshi
 TITLE OF INVENTION: Antibody Against Human Interleukin-5
 Receptor Alpha Chain

NUMBER OF SEQUENCES: 106
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: Fast-SEQ Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/283,349
 FILING DATE: 29-Oct-2002
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/836,561
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: JP 232384/95
 FILING DATE: 11-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Lawrence, III, Stanton T
 REFERENCE NUMBER: 25.736
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-790-9090
 TELEFAX: 212-669-9741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 137 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 31:

US-10-283-349-31

Query Match 79.6%; Score 593.5; DB 15; Length 137;

Best Local Similarity 82.9%; Pred. No. 2.9e-52;

Matches 116; Conservative 6; Mismatches 13; Indels 5; Gaps 1;

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 Db 1 MKCSWVMAFFLMAVVGVNSEVQLOQSGAELVKPGASVKSCTASSENFNIKDTYHCKQRP 60QY 61 EQGLEWIGRIDPANGTYKDPKFQGRATITADTSNTAYQLQSSLTSEDTAVYFCAREGY 120
 Db 61 EQGLEWIGRIDPANGTYKDPKFQGRATITADTSNTAYQLQSSLTSEDTAVYFCAREGY 120QY 61 EQGLEWIGRIDPANGTYKDPKFQGRATITADTSNTAYQLQSSLTSEDTAVYFCAREGY 120
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 Db 121 YGNYGYAMDWQGQTSVY 140QY 117 -GGLRLRFEDTYWGQGTLLTV 135
 Db 117 -GGLRLRFEDTYWGQGTLLTV 135RESULT 3
 US-10-056-794-15

Sequence 15, Application US/10056794

Publication No. US20030119078A1

GENERAL INFORMATION:

APPLICANT: Graves, Scott S.

Reno, John M.

Mallett, Robert W.

Hylarides, Mark D.

Searle, Stephen M.J.

Henry, Andrew H.

Pedersen, Jan T.

Rees, Anthony R.

TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT BIND TO THE

ANTIGEN BOUND BY ANTIBODY NR-LU-13 AND THEIR USE IN

PRETARGETING METHODS

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed IP Law Group

STREET: 701 Fifth Avenue, Suite 6300

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/056,794

FILING DATE: 24-Jan-2002

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey Ph.D., Richard G.

REGISTRATION NUMBER: 32,629

REFERENCE/DOCKET NUMBER: 690022.527C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 120 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GenCore version 5.1.6
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1 Protein - protein search, using sw model

run on: October 7, 2003, 09:09:40 ; Search time 19.798 Seconds
(without alignments)
680.050 Million cell updates/sec

title: US-09-155-739-4

perfect score: 746

sequence: 1 MKCSWWMMFLMAVVTGVNSE..... YGNYGVYAMDYWQGQTSYTV 140

product: 2

ALIGNMENT S

Query Match 80.0%; Score 597; DB 2; Length 136;
 Best Local Similarity 82.9%; Pred. No. 5.4e-45;
 Matches 116; Conservative 6; Mismatches 12; Indels 6; Gaps 1;

Qy 1 MKCSWVMMFFLMAVTVGNSEVQLOQGAAELYKPGASVQLSCTASGNFIKDTYIHCVKQRP 60
 Db 1 MKCSWVMMFFLMAVTVGNSEVQLOQGAAELYKPGASVQLSCTASGNFIKDTYIHCVKQRP 60

Qy 61 EQGLEWIGRIDPANGTYKDPKFQGKATIDATSSNTAYLQLSSLTSEDATAVYFCREGY 120
 Db 61 EQGLEWIGRIDPANGTYKDPKFQGKATIDATSSNTAYLQLSSLTSEDATAVYFCREGY 120

Qy 121 YGNYGTYAMDYWGQTSVTV 140
 Db 121 YGNYGTYAMDYWGQTSVTV 134

RESULT 5

S03471 Ig heavy chain V-D-J region (hybridoma G5 Bb 2.2) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 *text_change 20-Jun-2000
 C;Accession: S03471; S07453
 R;Rocca-Serra, J.; Matthes, H.W.; Raartinen, M.; Milstein, C.; These, J.; Fougerneau, R;Berdzo, J.; Krahenbuhl, J.-P.
 A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-hypervariable regions.
 A;Reference number: S03471; MUID:84057768; PMID:6416834
 A;Accession: S03471
 A;Molecule type: mRNA
 A;Residues: 7-120 <ROC1>
 A;Cross-references: EMBL:X01820; NID:951833; PID:91333983
 A;Note: this sequence was determined from the differentiated gene
 R;Rocca-Serra, J.; Mazine, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; These, J.; Fougerneau, J.; Immunol, 129, 254-258, 1982
 A;Title: The limited diversity of the mouse gamma chains anti-GAT repertoire does not
 A;Accession: S07453
 A;Molecule type: protein
 A;Residues: 1-13 <ROC2>
 C;Superfamily: immunoglobulin V region; immunoglobulin F;15-98/Domain: immunoglobulin F;15-115/Domain: immunoglobulin homology <IMM>

Query Match 76.5%; Score 570.5; DB 2; Length 137;
 Best Local Similarity 81.4%; Pred. No. 1.1e-42;
 Matches 114; Conservative 6; Mismatches 15; Indels 5; Gaps 2;

Qy 1 MKCSWVMMFFLMAVTVGNSEVQLOQGAAELYKPGASVQLSCTASGNFIKDTYIHCVKQRP 60
 Db 1 MKCSWVMMFFLMAVTVGNSEVQLOQGAAELYKPGASVQLSCTASGNFIKDTYIHCVKQRP 60

Qy 61 EQGLEWIGRIDPANGTYKDPKFQGKATIDATSSNTAYLQLSSLTSEDATAVYFCREGY 120
 Db 61 EQGLEWIGRIDPANGTYKDPKFQGKATIDATSSNTAYLQLSSLTSEDATAVYFCREGY 117

Qy 121 YGNYGTYAMDYWGQTSVTV 140
 Db 121 YGNYGTYAMDYWGQTSVTV 135

RESULT 4

PH1403 Ig heavy chain V region (clone micro m-46-6, 46-12) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Dete: 31-Dec-1993 #sequence_revision 31-Dec-1993 *text_change 21-Jan-2000
 C;Accession: PH1403
 R;Shirawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Ta
 J. Exp. Med. 176, 1209-1214, 1992
 A;Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in
 a virus.
 A;Reference number: PH1403; MUID:93018837; PMID:1402663
 A;Accession: PH1403
 A;Molecule type: DNA
 A;Residues: 1-123 <SH1>
 C;Genetics:
 A;Introns: 16;1
 C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 72.3%; Score 539; DB 2; Length 120;
 Best Local Similarity 89.3%; Pred. No. 5.3e-40;
 Matches 108; Conservative 7; Mismatches 2; Indels 4; Gaps 1;

Qy 20 EQVLOQSGAELYKPGASVQLSCTASGNFIKDTYIHCVKQRPQGLENTIGRIDPANGTYK 79
 Db 1 EQVLOQSGAELYKPGASVQLSCTASGNFIKDTYIHCVKQRPQGLENTIGRIDPANGTYK 60

Qy 80 DPKFQGKATIDATSSNTAYLQLSSLTSEDATAVYFCAREGYTGNYGTYAMDYWGQTSVTV 139
 Db 61 DPKFQGKATIDATSSNTAYLQLSSLTSEDATAVYFCAREGYTGNYGTYAMDYWGQTSVTV 116

Qy 140 V 140
 Db 117 V 117

RESULT 6

S17586 Ig heavy chain V region (E8) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Dete: 22-Nov-1993 #sequence_revision 26-May-1995 *text_change 21-Jan-2000
 C;Accession: S17586
 R;Myllyganan, S.E.; Patterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff, E.D.
 J. Mol. Biol. 221, 455-462, 1991
 A;Title: Biochemical implications from the variable gene sequences of an anti-cytochr
 forms.
 A;Reference number: S17586; MUID:92015240; PMID:1656053
 A;Accession: S17586
 A;Status: preliminary

Scoring table: BL050M62
Gapop 10.0 , Gapext 0.5
Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Result No.	Score	Query	Match	Length	DB	ID	Description
1	46.5	62.3	139	1	HV07_MOUSE	P01751	mus musculu
2	45.9	61.5	140	1	HV02_MOUSE	P01746	mus musculu
3	42.5	57.0	120	1	HV03_MOUSE	P01747	mus musculu
4	42.5	56.6	137	1	HV11_MOUSE	P01755	mus musculu
5	41.6	55.8	138	1	HV48_MOUSE	P03980	mus musculu
6	41.1	55.1	117	1	HV05_MOUSE	P01753	mus musculu
7	39.6	53.1	136	1	HV15_MOUSE	P01759	mus musculu
8	39.3	52.7	117	1	HV06_MOUSE	P01750	mus musculu
9	39.3	52.7	117	1	HV49_MOUSE	P06328	mus musculu
10	38.9	52.1	117	1	HV10_MOUSE	P01754	mus musculu
11	38.8	52.0	117	1	HV04_MOUSE	P01748	mus musculu
12	38.1	51.1	117	1	HV52_MOUSE	P06327	mus musculu
13	37.9	50.8	117	1	HV13_MOUSE	P01757	mus musculu
14	37.9	50.8	121	1	HV01_MOUSE	P01745	mus musculu
15	37.8	50.7	147	1	HV1C_HUMAN	P01744	homo sapien
16	37.4	50.1	117	1	HV05_MOUSE	P01749	mus musculu
17	37.4	50.1	117	1	HV12_MOUSE	P01756	mus musculu
18	37.2	49.9	117	1	HV14_MOUSE	P01758	mus musculu
19	368.5	49.4	118	1	HV51_MOUSE	P06330	mus musculu
20	367.	49.2	117	1	HV1B_HUMAN	P01743	homo sapien
21	360.5	48.3	120	1	HV50_MOUSE	P06329	mus musculu
22	359	48.1	117	1	HV1G_HUMAN	P23083	homo sapien
23	356.5	47.8	136	1	HV16_MOUSE	P01783	mus musculu
24	321.5	43.1	114	1	HV00_MOUSE	P01741	mus musculu
25	316.5	42.4	119	1	HV38_MOUSE	P01808	mus musculu
26	315	42.2	117	1	HV42_MOUSE	P01812	mus musculu
27	314	42.1	117	1	HV1A_HUMAN	P01742	homo sapien
28	312.5	41.9	119	1	HV37_MOUSE	P01807	mus musculu
29	311	41.7	142	1	HV01_FAT	P01805	ratmus norv
30	310.5	41.6	119	1	HV04_MOUSE	P01810	mus musculu
31	304	40.8	118	1	HV39_MOUSE	P01809	mus musculu
32	297	39.8	137	1	HV46_MOUSE	P01822	mus musculu
33	297	39.8	144	1	HV26_MOUSE	P01795	mus musculu

ALIGNMENTS

34	293.5	39.3	120	1	HV1H_HUMAN	P80421	homo sapien
35	292	39.1	117	1	HV11_MOUSE	P01811	mus musculu
36	291.5	39.1	116	1	HV05_CARAB	P19181	carassius a
37	290	38.9	123	1	HV16_MOUSE	P01806	mus musculu
38	290	38.9	123	1	HV24_MOUSE	P01793	mus musculu
39	288	38.6	117	1	HV3C_HUMAN	P01764	homo sapien
40	285.5	38.3	116	1	HV37_HUMAN	P01781	homo sapien
41	284.5	38.1	122	1	HV3G_MOUSE	P01768	homo sapien
42	284	38.1	144	1	HV3_MOUSE	P01819	mus musculu
43	284	38.1	146	1	HV22_HUMAN	P06331	homo sapien
44	283.5	37.9	122	1	HV2A_HUMAN	P01762	homo sapien
45	282	37.8	125	1	HV1F_HUMAN	P06326	homo sapien

RESULT 1
HV07_MOUSE STANDARD PRT: 139 AA.
ID HV07_MOUSE STANDARD PRT: 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NBP family of
cell 24:655-637 (1986).
RL CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN mRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPEN (4-HYDROXY-3-NITROPHENYL)ACETYL
(NPB ANTIBODIES).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announces/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; J00529; AAA38170.1; -.
DR PIR; J00529; MHMS18
DR PIR; J00801; MHMS18
DR PDB; 1A6U; 27-MAY-98.
DR PDB; 1A6W; 15-JUL-98.
DR InterPro; IPR00710; Ig-like.
DR InterPro; IPR03006; Ig_MHC.
DR InterPro; IPR03596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS05035; Ig_LINE; 1.
DR Immunoglobulin_V region; Signal; 3D-structure.
KW Ig HEAVY CHAIN V REGION B1-8/186-2.
FT SIGNAL 1 19
FT CHAIN 20 139
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DOMAIN 118 124
FT DOMAIN 125 139
FT DOMAIN 41 115
FT DISULFID 41 139
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Result No.	Score	Query Match	Length	DB ID	Description
1	562	100.0	106	16	AAR81321 Humanized anti-VLA 4
2	562	100.0	106	18	AARW2412 Humanised alpha-4
3	562	100.0	126	18	AARW2419 Humanised alpha-4
4	508	90.4	106	16	AAR81328 Mouse anti-VLA-4 a
5	508	90.4	126	16	AAR81326 Mouse anti-VLA-4 antibody
6	508	90.4	126	16	AAR81332 Human VLA-4 receptor
7	508	90.4	126	18	AARW22409 Alpha 4 integrin m
8	488	86.8	359	20	AAY29913 Human MCP-3 and mu
9	488	86.8	361	20	AAY29912 Human IP-10 and mu

QY 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWWQQTPGKAPRLLIHTSALQGIPS 60
 1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWWQQTPGKAPRLLIHTSALQGIPS 60
 1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 RFSGSGSGRDTFTTISQPEDIATYCLQYDNLWTFGGQTKEIK 106
 1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 61 RFSGSGSGRDTFTTISQPEDIATYCLQYDNLWTFGGQTKEIK 106
 1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 2
 PCT-US95-01219-7
 Sequence 7, Application PC/TUS9501219

; GENERAL INFORMATION:
 ; APPLICANT: Bendifig, Mary M.
 ; APPLICANT: Leger, Olivier J.
 ; APPLICANT: Saldana, Jose
 ; APPLICANT: Jones, S. Tarran
 ; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
 ; TITLE OF INVENTION: Adhesion Molecule VLA-4
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; STREET: Townsend and Townsend Khourie and Crew
 ; CITY: One Market Plaza, Steuart Tower, Suite 2000
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/561,521
 ; FILING DATE: 25-JAN-1994
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/186,269A
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William L.
 ; FILING DATE: 25-JAN-1994
 ; REGISTRATION NUMBER: 30,223
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-543-9600
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 106 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-561-521-5

Query Match 90.4%; Score 508; DB 2;
 Best Local Similarity 88.7%; Pred. No. 1.7e-40;
 Matches 94; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

TELEFAX: 415-543-5043
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 106 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US95-01219-7

Query Match 100.0%; Score 562; DB 5; Length 106;
 Best Local Similarity 100.0%; Pred. No. 1.6e-45;
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWWQQTPGKAPRLLIHTSALQGIPS 60
 1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWWQQTPGKAPRLLIHTSALQGIPS 60
 1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 RFSGSGSGRDTFTTISQPEDIATYCLQYDNLWTFGGQTKEIK 106
 1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 61 RFSGSGSGRDTFTTISQPEDIATYCLQYDNLWTFGGQTKEIK 106
 1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 3
 US-08-561-521-5
 ; Sequence 5, Application US/08561521
 ; Patent No. 5840299

GENERAL INFORMATION:
 ; APPLICANT: Bendifig, Mary M.
 ; APPLICANT: Leger, Olivier J.
 ; APPLICANT: Saldana, Jose
 ; APPLICANT: Jones, S. Tarran
 ; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
 ; TITLE OF INVENTION: Adhesion Molecule VLA-4
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; STREET: Townsend and Townsend Khourie and Crew
 ; CITY: One Market Plaza, Steuart Tower, Suite 2000
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/561,521
 ; FILING DATE: 25-JAN-1994
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/186,269A
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, William L.
 ; FILING DATE: 25-JAN-1994
 ; REGISTRATION NUMBER: 30,223
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-543-5043
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 106 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-561-521-5

Query Match 90.4%; Score 508; DB 2;
 Best Local Similarity 88.7%; Pred. No. 1.7e-40;
 Matches 94; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWWQQTPGKAPRLLIHTSALQGIPS 60
 1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWWQQTPGKAPRLLIHTSALQGIPS 60
 1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 RFSGSGSGRDTFTTISQPEDIATYCLQYDNLWTFGGQTKEIK 106
 1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 61 RFSGSGSGRDTFTTISQPEDIATYCLQYDNLWTFGGQTKEIK 106
 1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

GENERAL INFORMATION:
 ; APPLICANT: Bendifig, Mary M.
 ; APPLICANT: Leger, Olivier J.
 ; APPLICANT: Saldana, Jose
 ; APPLICANT: Jones, S. Tarran
 ; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
 ; TITLE OF INVENTION: Adhesion Molecule VLA-4
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; STREET: Townsend and Townsend Khourie and Crew
 ; CITY: One Market Plaza, Steuart Tower, Suite 2000
 ; STATE: California
 ; COUNTRY: USA

RESULT 2

US-10-335-394-13 ; Sequence 13, Application US/10335394 ; Publication No. US20030138452A1

GENERAL INFORMATION:

APPLICANT: Kwak, Larry

ORGANISM: Biragyn, Arya

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF FILE REFERENCE: 14014_0316/P

CURRENT APPLICATION NUMBER: US/10/335,394

PRIOR APPLICATION NUMBER: US/09/646,028

PRIOR FILING DATE: 2000-09-12

PRIOR APPLICATION NUMBER: 60/077,745

PRIOR FILING DATE: 1998-03-12

NUMBER OF SEQ ID NOS: 57

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 13

LENGTH: 361

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct

US-10-335-394-13

Query Match 86.8%; Score 488; DB 12; Length 361;

Best Local Similarity 84.9%; Pred. No. 8.7e-3;

Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Query 1 DIQMTQSPSSLSASVGDRVTITCKTSODINKYMAWQQTGKAPRLLIHTSALQGIPS 60

Db 235 DIQMTQSPSSLSASVGDRVTITCKTSODINKYMAWQQTGKAPRLLIHTSALQGIPS 294

Query 61 RFSGSGSGRDTFTTISLQPEDIATYCLQDNLYTFFGKVEIK 106

Db 295 RFSGSGSGRDTFSISNLEPEDIATYCLQDNLYTFFGKVEIK 340

RESULT 3

US-10-335-394-15 ; Sequence 15, Application US/10335394 ; Publication No. US20030138452A1

GENERAL INFORMATION:

APPLICANT: Kwak, Larry

ORGANISM: Biragyn, Arya

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF FILE REFERENCE: 14014_0316/P

CURRENT APPLICATION NUMBER: US/10/335,394

PRIOR APPLICATION NUMBER: US/09/646,028

PRIOR FILING DATE: 2000-09-12

PRIOR APPLICATION NUMBER: 60/077,745

PRIOR FILING DATE: 1998-03-12

NUMBER OF SEQ ID NOS: 57

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 15

LENGTH: 374

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct

US-10-335-394-15

Query Match 86.8%; Score 488; DB 12; Length 374;

Best Local Similarity 84.9%; Pred. No. 9.1e-3;

Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Query 1 DIQMTQSPSSLSASVGDRVTITCKTSODINKYMAWQQTGKAPRLLIHTSALQGIPS 60

Db 95 DIQMTQSPSSLSASVGDRVTITCKTSODINKYMAWQQTGKAPRLLIHTSALQGIPS 154

RESULT 4

US-09-229-200A-11 ; Sequence 11, Application US/09229200A ; Patent No. US2003009179A1

GENERAL INFORMATION:

APPLICANT: Jolliffe et al.

TITLE OF INVENTION: CD4 Specific Recombinant Antibody

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Johnson & Johnson Plaza

STREET: One Johnson & Johnson Plaza

CITY: New Brunswick

STATE: NJ

COUNTRY: USA

ZIP: 08933-7003

COMPUTER PREDIABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/229/200A

FILING DATE: 13-Jan-1999

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: John W. Wallen, III

REGISTRATION NUMBER: 35,403

REFERENCE/DOCKET NUMBER: ORT-948

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 524-2898

TELEFAX: (908) 524-2898

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 108

TYPE: amino acid

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-229-200A-11

Query Match 85.3%; Score 479.5; DB 9; Length 108;

Best Local Similarity 85.8%; Pred. No. 1.5e-36;

Matches 91; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

Query 1 D10MTQSPSSLSASVGDRVTITCKTSODINKYMAWQQTGKAPRLLIHTSALQGIPS 60

Db 1 D10MTQSPSSLSASVGDRVTITCKTSODINKYMAWQQTGKAPRLLIHTSALQGIPS 60

Query 61 RFSGSGSGRDTFTTISLQPEDIATYCLQDNLYTFFGKVEIK 105

Db 61 RFSGSGSGRDTFTTISLQPEDIATYCLQDNLYTFFGKVEIK 106

RESULT 5

US-09-229-200A-15 ; Sequence 15, Application US/09229200A ; Patent No. US2003009179A1

GENERAL INFORMATION:

APPLICANT: Jolliffe et al.

TITLE OF INVENTION: CD4 Specific Recombinant Antibody

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Johnson & Johnson Plaza

STREET: One Johnson & Johnson Plaza

CITY: New Brunswick

STATE: NJ

COUNTRY: USA

ZIP: 08933-7003

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 Compugen Ltd.
 OM protein - protein search, using sw model
 Run on: October 7, 2003, 09:09:40 ; Search time 14.9899 Seconds
 (without alignments)
 680.050 Million cell updates/sec

Title: US-09-155-739-7
 Perfect score: 562
 Sequence: 1 D1QMTQSPSSLASVGDRVT.....YCLQYDNLWTFQQGTVKEIK 106

Scoring table: BLOSUM62

Gappen 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR76:
 1: pir1:
 2: pir2:
 3: pir3:
 4: pir4:
 5: pir5:
 6: pir6:
 7: pir7:
 8: pir8:
 9: pir9:
 10: pir10:
 11: pir11:
 12: pir12:
 13: pir13:
 14: pir14:
 15: pir15:
 16: pir16:
 17: pir17:
 18: pir18:
 19: pir19:
 20: pir20:
 21: pir21:
 22: pir22:
 23: pir23:
 24: pir24:
 25: pir25:
 26: pir26:
 27: pir27:
 28: pir28:
 29: pir29:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	488	Ig kappa chain V r	S26330	104	2	Ig kappa chain V r
2	479	Ig kappa chain V r	S26330	104	2	Ig kappa chain V r
3	478	Ig kappa chain V r	C33936	106	2	Ig kappa chain V r
4	463.5	Ig kappa chain V r	S0365	125	2	Ig kappa chain - m
5	452	Ig kappa chain V r	PH1064	97	2	Ig light chain V r
6	446.5	Ig kappa chain V r	PL0270	107	2	Ig kappa chain V r
7	443.5	Ig kappa chain V r	1 KIHU	108	1	Ig kappa chain V-I
8	443.5	Ig kappa chain V r	S52789	129	2	Ig kappa chain V r
9	443	Ig kappa chain V r	S26332	103	2	Ig light chain V r
10	440	Ig kappa chain V r	PL0272	107	2	Ig kappa chain V r
11	440	Ig kappa chain V r	E33130	94	2	Ig kappa chain V r
12	439.5	Ig kappa chain V r	PL0269	107	2	Ig kappa chain V r
13	439.5	Ig kappa chain V r	PL0271	107	2	Ig kappa chain V r
14	439.5	Ig kappa chain V r	1 KIHU	108	1	Ig kappa chain V-I
15	435.5	Ig kappa chain V r	139154	108	2	Ig kappa chain (BR)
16	429.5	Ig kappa chain V r	41118	110	1	Ig kappa chain V-J
17	429.5	Ig kappa chain V r	S40367	127	2	Ig kappa chain V-J
18	426	Ig kappa chain V r	S36275	107	2	Ig lambda chain V
19	424.5	Ig kappa chain V r	S40333	125	2	Ig kappa chain V-J
20	421.5	Ig kappa chain V r	1 KIHU	108	1	Ig kappa chain V-I
21	419.5	Ig kappa chain V-I	1 KIHU	74.6	108	Ig kappa chain V-I
22	419.5	Ig kappa chain V-I	1 KIHU	74.6	108	Ig kappa chain V-I
23	418.5	Ig kappa chain - h	S40331	123	2	Ig kappa chain - h
24	415.5	Ig kappa chain - h	S31998	109	2	Ig kappa chain - h
25	415.5	Ig kappa chain - h	S4052	131	2	Ig kappa chain V-J
26	414	Ig kappa chain V-I	S40336	124	2	Ig kappa chain V-J
27	413.5	Ig kappa chain V-I	1 KIHU	73.6	108	Ig kappa chain V-I
28	412.5	Ig kappa chain V-I	B49047	73.4	108	Ig kappa chain V-I
29	412	Ig kappa chain V-I	PC2397	106	2	anti-tetanus toxin

RESULT 1

S26330

Ig kappa chain V region - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
 C;Accession: S26330
 R;Stark, S.E.; Caton, A.J., 1991
 J. Exp. Med. 174, 613-624, 1991
 A;Title: Antibodies that are specific for a single amino acid interexchange in a protein
 A;Reference number: S26309; MUID:9141421; PMID:1908510
 A;Accession: S26330
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-104 <SP>
 A;Cross-references: EMBL:X59185; PIDN:952116; PIDN:91334063
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin homology <IMM>
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.8%; Score 488; DB 2; Length 104;
 Best Local Similarity 85.6%; Pred. No. 1-6-35; 7: Indels 0; Gaps 0;

Qy 1 D1OMTQSPSSLASVGDRVTICKTCKASDINKYMAWYQTPGAPRLIHYTSLQPGIPS 60
 Db 1 D1OMTQSPSSLASVGDRVTICKTCKASDINKYMAWYQTPGAPRLIHYTSLQPGIPS 60
 Qy 61 RFSGSGSGRDYTFITSSQPEDIATYCLQYDNLWTFQGTKE 104
 Db 61 RFSGSGSGRDYTFITSSQPEDIATYCLQYDNLWTFQGTKE 104
 Qy 61 RFSGSGSGRDYFSISNLEPEDIATYCLQYDNLWTFQGTKE 104
 Db 61 RFSGSGSGRDYFSISNLEPEDIATYCLQYDNLWTFQGTKE 104

RESULT 2

S26329

Ig kappa chain V region - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
 C;Accession: S26329
 R;Stark, S.E.; Caton, A.J., 1991
 J. Exp. Med. 174, 613-624, 1991
 A;Title: Antibodies that are specific for a single amino acid interexchange in a protein
 A;Reference number: S26309; MUID:9141421; PMID:1908510
 A;Accession: S26329
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-104 <SP>
 A;Cross-references: EMBL:X59173; PIDN:952309; PIDN:91334059
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin homology
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.2%; Score 479; DB 2; Length 104;

Best Local Similarity 84.6%; Pred. No. 9.8e-35; Matches 88; Conservative 9; Mismatches 7; Indels 0; Gaps 0; Query 1 D1QMTQSPSSLSASVGDRYTFITKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
Db 1 D1QMTQSPSSLSASLGKVITCKASQDINKYTAWYQHKPGKGPRLIHYTSALQPGIPS 60
Qy 61 RFSGSGSGRDYTFITISLQPEIATYCYCLOYDNLTWFGGTKE 104
Db 61 RFSGSGSGRDYTFITISLQPEIATYCYCLOYDNLTWFGGTKE 104

RESULT 3
C33936 Ig kappa chain V region (VM13) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 *sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C;Accession: C33936
proc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989
A;Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene
A;Reference number: A33936; MUID:89282831; PMID:2471975
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-106 <HEE>
A;Cross References: GB:J04577; NID:9623187; PID:AAA60443.1; PID:g623189
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.1%; Score 478; DB 2; Length 106;
Best Local Similarity 83.0%; Pred. No. 1.2e-34;
Matches 88; Conservative 10; Mismatches 8; Indels 0; Gaps 0;
Query 1 D1QMTQSPSSLSASVGDRYTFITKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
Db 1 D1QMTQSPSSLSASLGKVITCKASQDINKYTAWYQHKPGKGPRLIHYTSALQPGIPS 60
Qy 61 RFSGSGSGRDYTFITISLQPEIATYCYCLOYDNLTWFGGTKE 106
Db 61 RFSGSGSGRDYTFITISLQPEIATYCYCLOYDNLTWFGGTKE 106

RESULT 4
S09365 Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 *sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S09365
Nucleic Acids Res. 17, 9797-9809, 1989
A;Title: Direct evidence for intrstrand DNA inversion of kappa immunoglobulin gene segment
A;Reference number: S09365; MUID:90098844; PMID:2513557
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-125 <FED>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 463.5; DB 2; Length 125;
Best Local Similarity 83.2%; Pred. No. 2.6e-33;
Matches 89; Conservative 7; Mismatches 10; Indels 1; Gaps 1;
Query 1 D1QMTQSPSSLSASVGDRYTFITKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
Db 18 D1QMTQSPSSLSASLGKVITCKASQDINKYTAWYQHKPGKGPRLIHYTSALQPGIPS 77
Qy 61 RFSGSGSGRDYTFITISLQPEIATYCYCLOYDNLTWFGGTKE 106
Db 78 RFSGSGSGSDYTFITISLQPEIATYCYCLOYDNLTWFGGTKE 124

RESULT 5
PH1064 Ig light chain V region (clone 202.54) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 *sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1064
R;Tillman, D. M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1064
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-97 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 452; DB 2; Length 97;
Best Local Similarity 85.6%; Pred. No. 2e-32;
Matches 83; Conservative 8; Mismatches 6; Indels 0; Gaps 0;
Qy 1 D1QMTQSPSSLSASVGDRYTFITKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
Db 1 D1QMTQSPSSLSASLGKVITCKASQDINKYTAWYQHKPGKGPRLIHYTSALQPGIPS 60
Qy 61 RFSGSGSGRDYTFITISLQPEIATYCYCLOYDNLTWFGGTKE 97
Db 61 RFSGSGSGRDYTFITISLQPEIATYCYCLOYDNLTWFGGTKE 97

RESULT 6
PL0270 Ig kappa chain V region (anti-DNA, 6G6V) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 *sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0270
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-271, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat.
A;Reference number: PL0231; MUID:9011618; PMID:2104919
A;Accession: PL0270
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4

Query Match 79.4%; Score 446.5; DB 2; Length 107;
Best Local Similarity 79.4%; Pred. No. 6.5e-32;
Matches 85; Conservative 11; Mismatches 10; Indels 1; Gaps 1;
Qy 1 D1QMTQSPSSLSASVGDRYTFITKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
Db 1 D1QMTQSPSCSLSASLGDKYITCIRPSQDISKNAWYQHAGKGPRLIHYTSALQPGIPS 60
Qy 61 RFSGSGSGRDYTFITISLQPEIATYCYCLOYDNLTWFGGTKE 106
Db 61 RFSGSGSGSDYTFITISLQPEIATYCYCLOYDNLTWFGGTKE 107

RESULT 7
K1HURE

Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5		
Searched:	127863 seqs, 47026705 residues			
Total number of hits satisfying chosen parameters:	127863			
Minimum DB seq length:	0			
Maximum DB seq length:	2000000000			
Post-processing:	Minimum Match 0%	Maximum Match 100%		
Database :	SwissProt_41:	Listing first 45 summaries		
			Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
			SUMMARIES	
Result No.	Score	Query	Match Length DB ID Description	
1	443.5	KV10_HUMAN	78.9 108 1 KV10_HUMAN	P01607 homo sapien
2	439.5	KV1B_HUMAN	78.2 108 1 KV1B_HUMAN	P01594 homo sapien
3	421.5	KV1M_HUMAN	75.0 108 1 KV1M_HUMAN	P01605 homo sapien
4	419.5	KV1A_HUMAN	74.6 108 1 KV1A_HUMAN	P01593 homo sapien
5	419.5	KV1P_HUMAN	74.6 108 1 KV1P_HUMAN	P01608 homo sapien
6	419.5	KV1Y_HUMAN	74.6 108 1 KV1Y_HUMAN	P00362 homo sapien
7	413.5	KV1Q_HUMAN	73.6 108 1 KV1Q_HUMAN	P01609 homo sapien
8	409.5	KV1D_HUMAN	72.9 129 1 KV1D_HUMAN	P04431 homo sapien
9	409.5	KV1R_HUMAN	72.8 107 1 KV1R_HUMAN	P01596 homo sapien
10	408.5	KV1L_HUMAN	72.7 108 1 KV1L_HUMAN	P01610 homo sapien
11	402.5	KV1H_HUMAN	71.6 108 1 KV1H_HUMAN	P01600 homo sapien
12	397.5	KV1F_HUMAN	70.7 108 1 KV1F_HUMAN	P01598 homo sapien
13	396.5	KV1N_HUMAN	70.6 108 1 KV1N_HUMAN	P04430 homo sapien
14	390.5	KV1K_HUMAN	69.5 108 1 KV1K_HUMAN	P01603 homo sapien
15	388.5	KV1E_HUMAN	69.1 108 1 KV1E_HUMAN	P01597 homo sapien
16	386.5	KV1L_HUMAN	68.8 108 1 KV1L_HUMAN	P01604 homo sapien
17	385.5	KV1N_HUMAN	68.6 108 1 KV1N_HUMAN	P01606 homo sapien
18	384.5	KV1C_HUMAN	68.4 108 1 KV1C_HUMAN	P01595 homo sapien
19	383.5	KV1G_HUMAN	68.2 108 1 KV1G_HUMAN	P01599 homo sapien
20	383.5	KV1X_HUMAN	68.2 129 1 KV1X_HUMAN	P04432 homo sapien
21	381.5	KV1S_HUMAN	67.9 108 1 KV1S_HUMAN	P01611 homo sapien
22	376.5	KV4C_HUMAN	67.0 134 1 KV4C_HUMAN	P06314 homo sapien
23	371.5	KV5J_MOUSE	66.1 108 1 KV5J_MOUSE	P01643 mus musculu
24	368	KV1J_HUMAN	65.5 117 1 KV1J_HUMAN	P01602 homo sapien
25	366.5	KV5E_MOUSE	65.2 128 1 KV5E_MOUSE	P01637 mus musculu
26	365	KV4B_HUMAN	64.9 133 1 KV4B_HUMAN	P06313 homo sapien
27	364.5	KV5O_MOUSE	64.9 108 1 KV5O_MOUSE	P01648 mus musculu
28	363.5	KV5N_HUMAN	64.7 108 1 KV5N_HUMAN	P01647 mus musculu
29	362	KV5J_MOUSE	64.4 109 1 KV5J_MOUSE	P01612 homo sapien
30	362	KV1L_HUMAN	64.4 117 1 KV1L_HUMAN	P01601 homo sapien
31	361.5	KV5K_MOUSE	64.3 108 1 KV5K_MOUSE	P01644 mus musculu
32	359.5	KV5M_MOUSE	64.0 108 1 KV5M_MOUSE	P01646 mus musculu
33	358.5	KV5L_MOUSE	63.8 109 1 KV5L_MOUSE	P01645 mus musculu

FT	STRAND	10	13	DR	InterPro; IPR003006; IG_MHC.
FT	TURN	15	16	DR	InterPro; IPR003596; Ig_V.
FT	STRAND	19	25	DR	Pfam; PF00047; Ig_V.
FT	TURN	30	31	DR	SMART; SM00406; IgV.
FT	STRAND	33	38	DR	PROSITE; PS5085; Ig_LIKE.
FT	TURN	40	41	KW	Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT	STRAND	44	49	FT	PROSITE; PS5085; Ig_LIKE.
FT	TURN	50	52	FT	Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT	STRAND	53	54	FT	COMPLEMENTARITY-DETERMINING-1.
FT	TURN	56	57	FT	COMPLEMENTARITY-DETERMINING-2.
FT	TURN	60	61	FT	COMPLEMENTARITY-DETERMINING-3.
FT	STRAND	62	67	FT	COMPLEMENTARITY-DETERMINING-4.
FT	TURN	68	69	FT	BY SIMILARITY.
FT	STRAND	70	75	FT	DISULFID
FT	HELIX	80	82	FT	NON-TER
FT	STRAND	85	90	SQ	SEQUENCE
FT	STRAND	97	98	108 AA;	11939 MW;
FT	STRAND	102	106	85;	E8011187EB6F6FB9 CRC64;
FT	NON-TER	108	108	86;	Query Match
SQ	SEQUENCE	108 AA;	11902 MW;	Best Local Similarity	Score 43.5; DB 1; Length 108;
				Matches 9;	Pred. No. 4.9e-40;
				Mismatches 10;	Indels 1; Gaps 1;
					Best Local Similarity 81.1%; Pred. No. 4.9e-40;
					Matches 9;
					Conservative 8;
					Mismatches 13;
					Indels 1; Gaps 1;
QY	1	1	1	Qy	1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRILHYTSALORGIPS 60
Db	1	1	1	Db	1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRILHYTSALORGIPS 60
QY	61	61	61	Qy	61 RFSGSGSGRDTFTISSLOPEDIATYCLQYDNL-WTEGQGTYK 106
Db	61	61	61	Db	61 RFSGSGSGRDTFTISSLOPEDIATYCLQYDNL-WTEGQGTYK 106
RESULT 3					
KV1M_HUMAN					
ID	KV1M_HUMAN	STANDARD;	PRT;	STANDARD;	PRT;
AC	AC	106 AA.	108 AA.	106 AA.	108 AA.
DT	PO1594;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-SEP-2003 (Rel. 42, Last annotation update)				
DE	19 kappa chain V-I region AU.				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
RN	[1]				
RN	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE			RT	Complete amino acid sequence of the variable domains of two human
RX	MDLINE-72189444; PubMed-5028201;			RT	IGM anti-gamma globulins (IgY/IgM) with shared idotypic
RA	R			RT	specificities ";
RA	Schietrich R., Hirschmann N.;			RL	Scand. J. Immunol. 5:677-684 (1976).
RT	"Rule of antibody structure. The primary structure of a monoclonal			CC	-1- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
RT	immunoglobulin L chain of the kappa type, subgroup I (Bence-Jones			CC	CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-IIII Kappa CHAIN,
RT	protein Au.";			CC	WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
RL	Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).			CC	-1 - MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
RL	[2]			CC	GLOBULIN ACTIVITY.
RP	X-RAY CRYSTALLOGRAPHY			DR	PIR; A01871; KIHLU.
RX	MDLINE-77022433; PubMed-1234024;			DR	HSPP; P01607; IRI.
RA	Fehlhammer H., Schiffer M., Epp O., Colman P. M., Lattman E. E.,			DR	GO; GO:0005576; C:extracellular; NAS.
RA	Schwarzger P., Steigemann W., Schramm H.J.;			DR	GO; GO:000323; P:antigen binding activity; NAS.
RT	"The structure determination of the variable portion of the			DR	GO; GO:0006935; P:immune response; NAS.
RT	Bence-Jones protein Au.";			DR	InterPro; IPR007110; Ig-like.
RL	Biophys. Struct. Mech. 1:139-146(1975).			DR	InterPro; IPR003006; Ig_MRC.
RL	[2]			DR	InterPro; IPR003516; Ig_V.
CC	-1 - MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY			DR	Pfam; PF00047; Ig_V.
CC	MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V			DR	SMART; SM00406; Ig_V.
CC	REGION OF THE KAPPA CHAIN REL.			DR	PROSITE; PS50835; Ig_LIKE.
CC	-1 - MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.			KW	Immunoglobulin V region.
DR	Pfam; A91653; KIHLU.			FT	PROSITE; PS50835; Ig_LIKE.
DR	PDB; 1TY5; 30-JAN-02.			FT	COMPLEMENTARITY-DETERMINING-1.
DR	GO; GO:0005576; C:extracellular; NAS.			FT	COMPLEMENTARITY-DETERMINING-2.
DR	GO; GO:0003833; P:antigen binding activity; NAS.			FT	COMPLEMENTARITY-DETERMINING-3.
DR	GO; GO:0006935; P:immune response; NAS.			FT	FRAMWORK-3.
DR	InterPro; IPR007110; Ig-like.			FT	COMPLEMENTARITY-DETERMINING-3.

Result No.	Score	Query	Match	Length	DB	ID	Description
1	428.5	76.2	108	4	Q9UL77		Q9UL77 homo sapien
2	418	74.4	241	11	Q921a6		Q921a6 mus musculu
3	414	73.7	107	4	Q96sa9		Q96sa9 homo sapien
4	406.5	72.3	108	4	Q9UL70		Q9UL70 homo sapien
5	395	70.3	107	4	Q9UL81		Q9UL81 homo sapien
6	385.5	68.6	108	4	Q9UL79		Q9UL79 homo sapien
7	384.5	68.4	214	11	Q9RIAS		Q9RIAS mus musculu
8	379.5	67.5	233	11	Q91WS9		Q91WS9 mus musculu
9	369.5	65.7	234	11	Q9R062		Q9R062 mus musculu
10	365.5	65.0	116	4	Q96PF6		Q96PF6 homo sapien
11	362.5	64.5	107	4	Q9UL74		Q9UL74 mus musculu
12	355.5	63.3	234	11	Q9JW8		Q9JW8 mus musculu
13	353.5	62.9	109	11	Q920E6		Q920E6 mus musculu
14	342.5	60.9	234	4	Q8NEK1		Q8NEK1 homo sapien
15	337.5	60.1	298	11	Q9QYF0		Q9QYF0 mus musculu
16	336.5	59.9	108	4	Q9UL83		Q9UL83 homo sapien

ALIGNMENTS

RESULT 1

Q9UL77	PRELIMINARY;	PRT;	108 AA.
ID Q9UL77;			
AC Q9UL77;			
DT 01-MAY-2000 (TREMBLrel. 13, Created)			
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE Myosin-reactive immunoglobulin light chain variable region (Fragment).			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=38277139; PubMed=9614934;			
RA Wu X., Liu B., Van der Merwe P.L., Kaliss N.N., Berney S.M., Young D.C.;			
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."			
RT Clin. Immunol. Immunopathol. 87:184-192(1998).			
DR EMBL; AF05037; AA05627.1; -.			
DR HSSP; P01607; 1REI.			
DR InterPro; IPR007110; Ig like.			
DR InterPro; IPR03006; Ig_MHC.			
DR InterPro; IPR003596; Ig_V.			
DR Pfam; PF00047; ig; 1.			
DR SMART; SM00406; IgV; 1.			
DR PROSITE; PS50835; Ig_LIKE; 1.			
DR NON_TER 1			
FT NON_TER 108 AA; 11738 MW; C06681716C4D16F3 CRC64;			
SQ SEQUENCE 108 AA;			

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Query	Match	Length	DB	ID	Description
1	428.5	76.2	108	4	Q9UL77		Q9UL77 homo sapien
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3	414	73.7	107	4	Q96sa9		Q96sa9 homo sapien
4	406.5	72.3	108	4	Q9UL70		Q9UL70 homo sapien
5	395	70.3	107	4	Q9UL81		Q9UL81 homo sapien
6	385.5	68.6	108	4	Q9UL79		Q9UL79 homo sapien
7	384.5	68.4	214	11	Q9RIAS		Q9RIAS mus musculu
8	379.5	67.5	233	11	Q91WS9		Q91WS9 mus musculu
9	369.5	65.7	234	11	Q9R062		Q9R062 mus musculu
10	365.5	65.0	116	4	Q96PF6		Q96PF6 homo sapien
11	362.5	64.5	107	4	Q9UL74		Q9UL74 mus musculu
12	355.5	63.3	234	11	Q9JW8		Q9JW8 mus musculu
13	353.5	62.9	109	11	Q920E6		Q920E6 mus musculu
14	342.5	60.9	234	4	Q8NEK1		Q8NEK1 homo sapien
15	337.5	60.1	298	11	Q9QYF0		Q9QYF0 mus musculu
16	336.5	59.9	108	4	Q9UL83		Q9UL83 homo sapien

Query Match Score 428.5%; DB 4; Length 108;
Best Local Similarity 76.6%; Fred. No. 5.1e-41;
Matches 8; Mismatches 8; Indels 1; Gaps 1;
1 DIQMTQSPSSLSASVGDRVTICKTSQDINKYMAWQQTPGKAPRLIHTSALQGIPS 60
Q9j182

Db	1	DIQMTQSPSSLASVGDRVTITCRASQISSYLNWYQQKPGKAPNLIIYASSILQSGVPS	60	DR EMBL; U96396; AAB68785; 1; -.
Qy	61	RFSGSGSGDFTTISLQPEDIATYCLQ-TDNLWTFGQQTKEIK 106		DR InterPro; IPR07110; Ig-like.
Db	61	RFSGSGSGDFTTISLQPEDIATYCLQ-TDNLWTFGQQTKEIK 107		DR InterPro; IPR03006; Ig_MHC.
RESULT 2				DR Pfam; PF00041; Ig_1.
Q92IA6		PRELIMINARY;	PRT;	DR SMART; SM00406; Igv; 1.
AC	Q92IA6;			DR PROSITE; PS50835; Ig_LIKE; 1.
DT	01-DEC-2001	(TREMBLrel. 19, Created)		FT NON_TER 1
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)		FT NON_TER 107
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)		SQ 107 AA; 11520 MW;
DE	Anti-CEA 79	single chain Fv fragment (Fragment).		Query Match 73.7%; Score 414; DB 4; Length 107;
OS	Mus musculus (Mouse).			Best Local Similarity 75.5%; Pred. No. 2.2e-39;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathia; Murinae; Mus; NCBI_TAXID=10090; [1]				Mismatches 9; Indels 0; Gaps 0;
OC				Matches 80; Conservative 17; Mismatches 17; Indels 0; Gaps 0;
OX				
RN		SEQUENCE FROM N.A.		
RX		Medline:981709426; PubMed:9509426;		
RA	Chung J.H., Choi S.J., Kim H.J., Kim I.-J., Choi I.-H., Lee S.D., YI K.S., Suh P.G., Ryu S.H., Chung H.K.;			
RA		"Cloning and characterization of cDNAs encoding VH and VL of a monoclonal anti-CEA antibody (CEA 79) cross reactive with NCA-95 and generation of a single chain Fv molecule (scFv).";		
RT		Cells : 816-819 (1997).		
RT		EMBL: U88067; ABA8044; 1;		
RT		InterPro; IPR007110; Ig-like.		
RT		InterPro; IPR013006; Ig_MHC.		
RT		InterPro; IPR03596; Ig_v.		
PFam; PF00047; Ig_2.		DR SMART; SM00406; Igv; 2.		
DR		DR PROSITE; PS50835; Ig_LIKE; 2.		
FT	NON_TER 1	FT NON_TER 241	241 AA; 26086 MW;	61 DIELTQSPSSLASVGDRVTITCRASQDINKYMWYQQTGKAPRLLIHYTSALQGIPS 60
FT				134 DIELTQSPSSLASVGDRVTITCRASQDINKYIANYQHKGKGRPSAHLIHYIQGIPS 193
FT				61 RFSGSGSGDFTTISLQPEDIATYCLQ-TDNLWTFGQQTKEIK 106
FT				194 RFSGSGSGDFTSISNLEPEDIATYCLHYDNLWTFGGTKEIK 239
SQ				*
Query Match 74.4%; Score 418; DB 11; Length 241;				
Best Local Similarity 73.6%; Pred. No. 2.2e-39;				
Matches 78; Conservative 12; Mismatches 16; Indels 0; Gaps 0;				
Qy	1	DIQMTQSPSSLASVGDRVTITCRASQDINKYMWYQQTGKAPRLLIHYTSALQGIPS 60		
Db	1	DIQMTQSPSSLASVGDRVTITCRASQDINKYIANYQHKGKGRPSAHLIHYIQGIPS 193		
Qy	1	DIELTQSPSSLASVGDRVTITCRASQDINKYIANYQHKGKGRPSAHLIHYIQGIPS 193		
Db	1	DIELTQSPSSLASVGDRVTITCRASQDINKYIANYQHKGKGRPSAHLIHYIQGIPS 193		
RESULT 3				
Q96SA9		PRELIMINARY;	PRT;	Score 406 5; DB 4; Length 108;
AC	Q96SA9;			
DT	01-DEC-2001	(TREMBLrel. 19, Created)		
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)		
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)		
DE	Anti-streptococcal/anti-myosin in immunoglobulin kappa light chain variable region (Fragment).			
OS	Homo sapiens (Human).			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo; NCBI_TAXID=9606; [1]				
OC				
OX				
RN		SEQUENCE FROM N.A.		
RX		Medline:98375899; PubMed:9712075;		
RA	Addresser E. E., Shikman A.R., Ward K.E., Cunningham M.W.;			
RT	Molecular analysis of polyclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin antibody. V region genes.			
RT	J. Immunol. 161:2020-2031(1998).			
RN		RESULT 5		
RX		Q9UL81	PRELIMINARY;	Score 406 5; DB 4; Length 107;
RA		ID Q9UL81	PRT;	Best Local Similarity 72.3%; Pred. No. 1.6e-38;
RT				Mismatches 12; Indels 1; Gaps 1;
RT				Matches 78; Conservative 12; Mismatches 16; Indels 1; Gaps 1;
RT				
RT				1 DIQMTQSPSSLASVGDRVTITCRASQDINKYIANYQHKGKGRPSAHLIHYIQGIPS 60
RT				1 DIQMTQSPSSLASVGDRVTITCRASQDINKYIANYQHKGKGRPSAHLIHYIQGIPS 60
RT				61 RFSGSGSGDFTTISLQPEDIATYCLQ-TDNLWTFGQQTKEIK 106
RT				61 RFSGSGSGDFTSISNLEPEDIATYCLHYDNLWTFGGTKEIK 239